

ДОПОЛНИТЕЛЬНЫЕ МАТЕРИАЛЫ

ЭКСПЕРИСЕНТАЛЬНЫЕ СТАТЬИ

ТРАНСКРИПТОМНЫЙ АНАЛИЗ ПОКОЯЩИХСЯ ЦИСТОПОДОБНЫХ КЛЕТОК *ESCHERICHIA COLI*

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Таблица S1. Картирование чтений на геном *E.coli* K12/MG1655 и количество чтений каждого гена, полученных после секвенатора (без домножения числа чтений для точки 1).

Table S1. Mapping of reads on the *E. coli* K12/MG1655 genome and the number of reads of each gene obtained after the sequencer (without multiplying the number of reads for point 1).

Gene	Start	End	Gene name	Gene product	Reads number	
					Point 1	Point 2
b0001	190	255	<i>thrL</i>	thr operon leader peptide	1	3
b0002	337	2799	<i>thrA</i>	Bifunctional aspartokinase/homoserine dehydrogenase 1	1770	2003
b0003	2801	3733	<i>thrB</i>	homoserine kinase	1173	802
b0004	3734	5020	<i>thrC</i>	L-threonine synthase	2293	1165
b0005	5234	5530	<i>yaaX</i>	DUF2502 family putative periplasmic protein	602	398
b0006	6459	5683	<i>yaaA</i>	peroxide resistance protein, lowers intracellular iron	755	465
b0007	7959	6529	<i>yaaJ</i>	putative transporter	637	704
b0008	8238	9191	<i>talB</i>	transaldolase B	61104	14545
b0009	9306	9893	<i>mog</i>	molybdochelatase incorporating molybdenum into molybdopterin	1844	482
b0010	10494	9928	<i>satP</i>	succinate-acetate transporter	406	526
b0011	11356	10643	<i>yaaW</i>	UPF0174 family protein	95	153
b0013	11786	11382	<i>yaaI</i>	UPF0412 family protein	20	53
b0014	12163	14079	<i>dnaK</i>	chaperone Hsp70, with co-chaperone DnaJ	127002	48999
b0015	14168	15298	<i>dnaJ</i>	chaperone Hsp40, DnaK co-chaperone	4209	2543
b0016	15445	16557	<i>insL1</i>	IS186 transposase	756	842
b0018	16960	16751	<i>mokC</i>	regulatory protein for HokC, overlaps CDS of hokC	147	94
b0019	17489	18655	<i>nhaA</i>	sodium-proton antiporter	2003	2576
b0020	18715	19620	<i>nhaR</i>	transcriptional activator of nhaA	966	2890
b0021	20314	19811	<i>insB1</i>	IS1 transposase B	721	1067
b0022	20508	20233	<i>insA</i>	IS1 repressor TnpA	96	513
b0023	21078	20815	<i>rpsT</i>	30S ribosomal subunit protein S20	4028	7330
b0024	21181	21399	<i>yaaY</i>	uncharacterized protein	5	26
b0025	21407	22348	<i>ribF</i>	bifunctional riboflavin kinase/FAD synthetase	1038	1242
b0026	22391	25207	<i>ileS</i>	isoleucyl-tRNA synthetase	10359	3520
b0027	25207	25701	<i>lspA</i>	prolipoprotein signal peptidase (signal peptidase II)	361	144
b0028	25826	26275	<i>fkpB</i>	FKBP-type peptidyl-prolyl cis-trans isomerase (rotamase)	534	180
b0029	26277	27227	<i>ispH</i>	4-hydroxy-3-methylbut-2-enyl diphosphate reductase, 4Fe-4S protein	1730	598
b0030	27293	28207	<i>rihC</i>	ribonucleoside hydrolase 3	1482	160
b0031	28374	29195	<i>dapB</i>	dihydrodipicolinate reductase	1099	597
b0032	29651	30799	<i>carA</i>	carbamoyl phosphate synthetase small subunit, glutamine amidotransferase	4031	2152
b0033	30817	34038	<i>carB</i>	carbamoyl-phosphate synthase large subunit	23169	2517
b0034	34300	34695	<i>caiF</i>	cai operon transcriptional activator	2029	736
b0035	35371	34781	<i>caiE</i>	stimulator of CaiD and CaiB enzyme activities	32	119
b0036	36162	35377	<i>caiD</i>	carnitiny-CoA dehydratase	16	31
b0037	37824	36271	<i>caiC</i>	putative crotonobetaine/carnitine-CoA ligase	158	271
b0038	39115	37898	<i>caiB</i>	crotonobetainyl CoA:carnitine CoA transferase	127	199
b0039	40386	39244	<i>caiA</i>	crotonobetaine reductase subunit II, FAD-binding	313	779
b0040	41931	40417	<i>caiT</i>	putative transporter	32	114
b0041	42403	43173	<i>fixA</i>	anaerobic carnitine reduction putative electron transfer flavoprotein subunit	37	24
b0042	43188	44129	<i>fixB</i>	putative electron transfer flavoprotein, NAD/FAD-binding domain and ETFP adenine nucleotide-binding domain-like protein	33	23
b0043	44180	45466	<i>fixC</i>	putative oxidoreductase	45	56

b0044	45463	45750	<i>fixX</i>	putative 4Fe-4S ferredoxin-type protein	3	6
b0045	45807	47138	<i>yaaU</i>	putative MFS sugar transporter; membrane protein	19	136
b0046	47246	47776	<i>kefF</i>	potassium-efflux system ancillary protein for KefC, glutathione-regulated; quinone oxidoreductase, FMN-dependent	234	157
b0047	47769	49631	<i>kefC</i>	potassium:proton antiporter	718	428
b0048	49823	50302	<i>folA</i>	dihydrofolate reductase	2428	2238
b0049	51222	50380	<i>apaH</i>	diadenosine tetraphosphatase	486	465
b0050	51606	51229	<i>apaG</i>	protein associated with Co2+ and Mg2+ efflux	1081	918
b0051	52430	51609	<i>rsmA</i>	16S rRNA m(6)A1518, m(6)A1519 dimethyltransferase, SAM-dependent	2324	1130
b0052	53416	52427	<i>pdxA</i>	4-hydroxy-L-threonine phosphate dehydrogenase, NAD-dependent	1250	1152
b0053	54702	53416	<i>surA</i>	peptidyl-prolyl cis-trans isomerase (PPIase)	9750	6377
b0054	57109	54755	<i>lptD</i>	LPS assembly OM complex LptDE, beta-barrel component	12524	10925
b0055	57364	58179	<i>djlA</i>	membrane-anchored DnaK co-chaperone, DNA-binding protein	410	426
b0058	60346	59687	<i>rluA</i>	dual specificity 23S rRNA pseudouridine(746), tRNA pseudouridine(32) synthase, SAM-dependent	626	507
b0059	63264	60358	<i>rapA</i>	RNA polymerase remodeling/recycling factor ATPase; RNA polymerase-associated, ATP-dependent RNA translocase	1608	833
b0060	65780	63429	<i>polB</i>	DNA polymerase II	369	709
b0061	66550	65855	<i>araD</i>	L-ribulose-5-phosphate 4-epimerase	54	51
b0062	68337	66835	<i>araA</i>	L-arabinose isomerase	206	89
b0063	70048	68348	<i>araB</i>	L-ribulokinase	201	67
b0064	70387	71265	<i>araC</i>	ara regulon transcriptional activator; autorepressor	1416	368
b0065	71351	72115	<i>yabI</i>	DedA family inner membrane protein	299	921
b0066	72927	72229	<i>thiQ</i>	thiamine/thiamine pyrophosphate ABC transporter ATPase	123	226
b0067	74521	72911	<i>thiP</i>	thiamine/thiamine pyrophosphate ABC transporter permease	78	177
b0068	75480	74497	<i>thiB</i>	thiamine/thiamine pyrophosphate/thiamine monophosphate ABC transporter periplasmic binding protein	176	358
b0069	77299	75644	<i>sgrR</i>	transcriptional DNA-binding transcriptional activator of sgrS sRNA	347	209
b0070	77621	78799	<i>setA</i>	broad specificity sugar efflux system	434	902
b0071	79453	78848	<i>leuD</i>	3-isopropylmalate dehydratase small subunit	293	694
b0072	80864	79464	<i>leuC</i>	3-isopropylmalate dehydratase large subunit	309	669
b0073	81958	80867	<i>leuB</i>	3-isopropylmalate dehydrogenase, NAD(+)-dependent	183	537
b0074	83529	81958	<i>leuA</i>	2-isopropylmalate synthase	225	1189
b0075	83708	83622	<i>leuL</i>	leu operon leader peptide	0	4
b0076	84368	85312	<i>leuO</i>	global transcription factor	140	1373
b0077	85630	87354	<i>ilvI</i>	acetolactate synthase 3 large subunit	603	739
b0078	87357	87848	<i>ilvH</i>	acetolactate synthase 3, small subunit, valine-sensitive	306	463
b0080	88028	89032	<i>cra</i>	transcriptional repressor-activator for carbon metabolism	5012	1229
b0081	89634	90092	<i>mraZ</i>	RsmH methyltransferase inhibitor	1661	2216
b0082	90094	91035	<i>rsmH</i>	16S rRNA m(4)C1402 methyltransferase, SAM-dependent	2517	1485
b0083	91032	91397	<i>ftsL</i>	membrane bound cell division leucine zipper septum protein	557	594
b0084	91413	93179	<i>ftsI</i>	transpeptidase involved in septal peptidoglycan synthesis; penicillin-binding protein 3	22090	75250
b0085	93166	94653	<i>murE</i>	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate:meso-diaminopimelate ligase	1923	953
b0086	94650	96008	<i>murF</i>	UDP-N-acetylmuramoyl-tripeptide:D-alanyl-D-alanine ligase	1880	914
b0087	96002	97084	<i>mraY</i>	phospho-N-acetylmuramoyl-pentapeptide transferase	991	416
b0088	97087	98403	<i>murD</i>	UDP-N-acetylmuramoyl-L-alanine:D-glutamate ligase	1902	634

b0089	98403	99647	<i>ftsW</i>	putative lipid II flippase; integral membrane protein; FtsZ ring stabilizer	1315	732
b0090	99644	100711	<i>murG</i>	N-acetylglucosaminyl transferase	965	770
b0091	100765	102240	<i>murC</i>	UDP-N-acetylmuramate:L-alanine ligase	2704	1264
b0092	102233	103153	<i>ddlB</i>	D-alanine:D-alanine ligase	3514	2487
b0093	103155	103985	<i>ftsQ</i>	divisome assembly protein, membrane anchored protein involved in growth of wall at septum	1935	2211
b0094	103982	105244	<i>ftsA</i>	ATP-binding cell division FtsK recruitment protein	3997	1782
b0095	105305	106456	<i>ftsZ</i>	GTP-binding tubulin-like cell division protein	14186	3260
b0096	106557	107474	<i>lpxC</i>	UDP-3-O-acyl N-acetylglucosamine deacetylase	31922	19101
b0097	107705	108217	<i>secM</i>	regulator of secA translation	1726	1809
b0098	108279	110984	<i>secA</i>	preprotein translocase subunit, ATPase	12911	3990
b0099	111044	111433	<i>mutT</i>	dGTP-preferring nucleoside triphosphate pyrophosphohydrolase	277	206
b0101	111846	111649	<i>yacG</i>	DNA gyrase inhibitor	312	148
b0102	112599	111856	<i>zapD</i>	FtsZ stabilizer	620	527
b0103	113219	112599	<i>coaE</i>	dephospho-CoA kinase	324	603
b0104	113444	114487	<i>guaC</i>	GMP reductase	6057	3373
b0106	115724	114522	<i>hofC</i>	assembly protein in type IV pilin biogenesis, transmembrane protein	97	445
b0107	117099	115714	<i>hofB</i>	T2SE secretion family protein; P-loop ATPase superfamily protein	140	701
b0108	117549	117109	<i>ppdD</i>	putative prepilin peptidase-dependent pilin	16	39
b0109	118645	117752	<i>nadC</i>	quinolinate phosphoribosyltransferase	2080	1226
b0110	118733	119284	<i>ampD</i>	1,6-anhydro-N-acetylmuramyl-L-alanine amidase, Zn-dependent; murein amidase	2076	945
b0111	119281	120135	<i>ampE</i>	ampicillin resistance inner membrane protein; putative signaling protein in beta-lactamase regulation	2589	435
b0112	121551	120178	<i>aroP</i>	aromatic amino acid transporter	1181	1228
b0113	122092	122856	<i>pdhR</i>	pyruvate dehydrogenase complex repressor; autorepressor	1136	737
b0114	123017	125680	<i>aceE</i>	pyruvate dehydrogenase, decarboxylase component E1, thiamine triphosphate-binding	70523	8592
b0115	125695	127587	<i>aceF</i>	pyruvate dehydrogenase, dihydrolipoyltransacetylase component E2	39212	3419
b0116	127912	129336	<i>lpd</i>	dihydrolipoyl dehydrogenase; E3 component of pyruvate and 2-oxoglutarate dehydrogenases complexes; glycine cleavage system L protein; dihydrolipoamide dehydrogenase	68420	12026
b0117	131260	129407	<i>yacH</i>	DUF3300 family protein	105	594
b0118	131615	134212	<i>acnB</i>	aconitate hydratase 2; aconitase B; 2-methyl-cis-aconitate hydratase	65055	13931
b0119	134388	134750	<i>yacL</i>	UPF0231 family protein	12210	3693
b0120	135582	134788	<i>speD</i>	S-adenosylmethionine decarboxylase	9984	5862
b0121	136464	135598	<i>speE</i>	spermidine synthase (putrescine aminopropyltransferase)	8862	2998
b0122	136917	136570	<i>yacC</i>	PulS_OutS family protein	318	1773
b0123	137083	138633	<i>cueO</i>	multicopper oxidase (laccase)	927	2921
b0124	141225	138835	<i>gcd</i>	glucose dehydrogenase	2302	1484
b0125	141431	141967	<i>hpt</i>	hypoxanthine phosphoribosyltransferase	1649	878
b0126	142670	142008	<i>can</i>	carbonic anhydrase	7470	4447
b0127	142779	143705	<i>yadG</i>	putative ABC transporter ATPase	1643	1203
b0128	143702	144472	<i>yadH</i>	putative ABC transporter permease	945	633
b0129	144577	145017	<i>yadI</i>	putative PTS Enzyme IIA	1750	462
b0130	145081	146310	<i>yadE</i>	putative polysaccharide deacetylase lipoprotein	548	1109
b0131	146694	146314	<i>panD</i>	aspartate 1-decarboxylase	5095	4579
b0132	146968	147870	<i>yadD</i>	transposase_31 family protein	234	4056
b0133	148795	147944	<i>panC</i>	pantothenate synthetase	4478	2186
b0134	149601	148807	<i>panB</i>	3-methyl-2-oxobutanoate hydroxymethyltransferase	2770	1008
b0135	150953	149715	<i>yadC</i>	putative fimbrial-like adhesin protein	93	1305

b0136	151599	151003	<i>yadK</i>	putative fimbrial-like adhesin protein	15	103
b0137	152231	151626	<i>yadL</i>	putative fimbrial-like adhesin protein	36	471
b0138	152812	152243	<i>yadM</i>	putative fimbrial-like adhesin protein	29	260
b0139	155426	152829	<i>htrE</i>	putative outer membrane usher protein	39	626
b0140	156201	155461	<i>yadV</i>	putative periplasmic pilin chaperone	7	123
b0141	156883	156299	<i>yadN</i>	putative fimbrial-like adhesin protein	20	74
b0142	157732	157253	<i>folK</i>	2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase	164	136
b0143	159126	157729	<i>pcnB</i>	poly(A) polymerase	1935	1324
b0144	160112	159186	<i>gluQ</i>	glutamyl-Q tRNA(Asp) synthetase	228	264
b0145	160604	160149	<i>dksA</i>	transcriptional regulator of rRNA transcription; DnaK suppressor protein	17224	5589
b0146	161486	160782	<i>sfsA</i>	sugar fermentation stimulation protein A	11907	5335
b0147	162031	161501	<i>ligT</i>	2'-5' RNA ligase	136	152
b0148	162105	164534	<i>hrpB</i>	putative ATP-dependent helicase	559	510
b0149	164730	167264	<i>mrcB</i>	fused glycosyl transferase and transpeptidase	2790	1241
b0150	167484	169727	<i>fhuA</i>	ferrichrome outer membrane transporter	7327	1525
b0151	169778	170575	<i>fhuC</i>	iron(3+)-hydroxamate import ABC transporter ATPase	270	45
b0152	170575	171465	<i>fhuD</i>	iron(3+)-hydroxamate import ABC transporter periplasmic binding protein	199	66
b0153	171462	173444	<i>fhuB</i>	iron(3+)-hydroxamate import ABC transporter permease	236	450
b0154	174882	173602	<i>hemL</i>	glutamate-1-semialdehyde aminotransferase (aminomutase)	3250	858
b0155	175107	176528	<i>clcA</i>	H(+)/Cl(-) exchange transporter	523	507
b0156	176610	176954	<i>erpA</i>	iron-sulfur cluster insertion protein	1909	3717
b0157	177624	177001	<i>yadS</i>	UPF0126 family inner membrane protein	110	405
b0158	178462	177662	<i>btuF</i>	vitamin B12 ABC transporter periplasmic binding protein	335	274
b0159	179153	178455	<i>mtn</i>	5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase	4622	2240
b0160	179237	180754	<i>dgt</i>	deoxyguanosine triphosphate triphosphohydrolase	1059	1026
b0161	180884	182308	<i>degP</i>	serine endoprotease (protease Do), membrane-associated	1350	6867
b0162	182463	183620	<i>cdaR</i>	carbohydrate diacid regulon transcriptional regulator; autoregulator	1852	1306
b0163	184095	183709	<i>yaeH</i>	UPF0325 family protein	19248	17146
b0164	185069	184257	<i>yaeI</i>	phosphodiesterase with model substrate bis-pNPP	144	712
b0166	185947	185123	<i>dapD</i>	2,3,4,5-tetrahydropyridine-2-carboxylate N-succinyltransferase	6289	2480
b0167	188650	185978	<i>glnD</i>	uridylyltransferase	2608	1282
b0168	189506	188712	<i>map</i>	methionine aminopeptidase	8706	3690
b0169	189874	190599	<i>rpsB</i>	30S ribosomal subunit protein S2	50711	14756
b0170	190857	191708	<i>tsf</i>	translation elongation factor EF-Ts	38778	9240
b0171	191855	192580	<i>pyrH</i>	uridylate kinase	2688	1731
b0172	192872	193429	<i>frr</i>	ribosome recycling factor	12742	3321
b0173	193521	194717	<i>dxr</i>	1-deoxy-D-xylulose 5-phosphate reductoisomerase	786	560
b0174	194903	195664	<i>ispU</i>	undecaprenyl pyrophosphate synthase	2033	2615
b0175	195677	196534	<i>cdsA</i>	CDP-diglyceride synthase	1189	1212
b0176	196546	197898	<i>rseP</i>	inner membrane zinc RIP metalloprotease; RpoE activator, by degrading RseA; cleaved signal peptide endoprotease	3616	8129
b0177	197928	200360	<i>bamA</i>	BamABCDE complex OM biogenesis outer membrane pore-forming assembly factor	24846	12919
b0178	200482	200967	<i>skp</i>	periplasmic chaperone	22973	4930
b0179	200971	201996	<i>lpxD</i>	UDP-3-O-(3-hydroxymyristoyl)-glucosamine N-acyltransferase	6246	4514
b0180	202101	202556	<i>fabZ</i>	(3R)-hydroxymyristol acyl carrier protein dehydratase	2778	2611
b0181	202560	203348	<i>lpxA</i>	UDP-N-acetylglucosamine acetyltransferase	2866	2099
b0182	203348	204496	<i>lpxB</i>	tetraacyldisaccharide-1-P synthase	753	1199

b0183	204493	205089	<i>rnhB</i>	ribonuclease HII, degrades RNA of DNA-RNA hybrids	430	222
b0184	205126	208608	<i>dnaE</i>	DNA polymerase III alpha subunit	3204	2366
b0185	208621	209580	<i>accA</i>	acetyl-CoA carboxylase, carboxytransferase, alpha subunit	4014	1990
b0186	209679	211820	<i>ldcC</i>	lysine decarboxylase 2, constitutive	1647	1227
b0187	211877	212266	<i>yaeR</i>	putative lyase	647	618
b0188	212331	213629	<i>tilS</i>	tRNA(Ile)-lysine synthetase	374	365
b0189	213932	213678	<i>rof</i>	modulator of Rho-dependent transcription termination	1269	526
b0190	214291	214836	<i>yaeQ</i>	PDDEXK superfamily protein	606	432
b0191	214833	215255	<i>arfB</i>	alternative stalled-ribosome rescue factor B; peptidyl-tRNA hydrolase, ribosome-attached	292	278
b0192	215269	215979	<i>nlpE</i>	lipoprotein involved with copper homeostasis and adhesion	777	678
b0193	217003	216179	<i>yaeF</i>	putative lipoprotein	89	683
b0194	218775	217057	<i>proS</i>	prolyl-tRNA synthetase	11968	2312
b0195	219594	218887	<i>tsaA</i>	tRNA-Thr(GGU) m(6)t(6)A37 methyltransferase, SAM-dependent	272	134
b0196	219995	219591	<i>rscF</i>	putative outer membrane protein	2693	1219
b0197	220928	220113	<i>metQ</i>	DL-methionine transporter subunit	13791	13658
b0198	221621	220968	<i>metI</i>	DL-methionine transporter subunit	878	943
b0199	222645	221614	<i>metN</i>	DL-methionine transporter subunit	1898	2291
b0200	222833	223408	<i>gmhB</i>	D,D-heptose 1,7-bisphosphate phosphatase	1575	1433
b0207	229167	229970	<i>dkgB</i>	2,5-diketo-D-gluconate reductase B	1363	704
b0208	230881	229967	<i>yafC</i>	LysR family putative transcriptional regulator	731	972
b0209	231122	231922	<i>yafD</i>	endo/exonuclease/phosphatase family protein	1338	1427
b0210	231926	232549	<i>yafE</i>	putative S-adenosyl-L-methionine-dependent methyltransferase	191	1884
b0211	233955	232597	<i>mltD</i>	putative membrane-bound lytic murein transglycosylase D	2321	27850
b0212	234782	234027	<i>gloB</i>	hydroxyacylglutathione hydrolase	997	1907
b0213	234816	235538	<i>yafS</i>	putative S-adenosyl-L-methionine-dependent methyltransferase	531	1178
b0214	236002	235535	<i>rnhA</i>	ribonuclease HI, degrades RNA of DNA-RNA hybrids	341	630
b0215	236067	236798	<i>dnaQ</i>	DNA polymerase III epsilon subunit	655	1232
b0217	237335	238120	<i>yafT</i>	lipoprotein	132	690
b0219	240189	239419	<i>yafV</i>	putative NAD(P)-binding C-N hydrolase family amidase	603	732
b0220	240343	240816	<i>ivy</i>	inhibitor of c-type lysozyme, periplasmic	2600	1153
b0221	243303	240859	<i>fadE</i>	acyl coenzyme A dehydrogenase	17563	12026
b0222	243543	244121	<i>gmhA</i>	D-sedoheptulose 7-phosphate isomerase	2823	857
b0223	244327	245094	<i>yafJ</i>	type 2 glutamine amidotransferase family protein	1033	621
b0224	245805	245065	<i>yafK</i>	L,D-transpeptidase-related protein	1626	5608
b0225	246239	245961	<i>yafQ</i>	mRNA interferase toxin of toxin-antitoxin pair YafQ/DinJ	295	3705
b0226	246502	246242	<i>dinJ</i>	antitoxin of YafQ-DinJ toxin-antitoxin system	1148	10482
b0227	246712	247461	<i>yafL</i>	putative lipoprotein and C40 family peptidase	48	286
b0228	247637	248134	<i>rayT</i>	RAYT REP element-mobilizing transposase; TnpA(REP)	646	355
b0231	250898	251953	<i>dinB</i>	DNA polymerase IV	439	968
b0232	252005	252298	<i>yafN</i>	antitoxin of the YafO-YafN toxin-antitoxin system	146	623
b0233	252301	252699	<i>yafO</i>	mRNA interferase toxin of the YafO-YafN toxin-antitoxin system	62	302
b0234	252709	253161	<i>yafP</i>	GNAT family putative N-acetyltransferase	51	241
b0237	255716	254259	<i>pepD</i>	aminoacyl-histidine dipeptidase (peptidase D)	16811	3717
b0238	255977	256435	<i>gpt</i>	xanthine phosphoribosyltransferase; xanthine-guanine phosphoribosyltransferase	1859	716
b0239	256527	257771	<i>frsA</i>	fermentation-respiration switch protein; PTS Enzyme IIA(Glc)-binding protein; pNP-butyrate esterase activity	1679	757
b0241	260100	259045	<i>phoE</i>	outer membrane phosphoporin protein E	9138	770
b0242	260388	261491	<i>proB</i>	gamma-glutamate kinase	1088	804

b0243	261503	262756	<i>proA</i>	gamma-glutamylphosphate reductase	2568	1347
b0245	263669	263328	<i>ykfI</i>	CP4-6 prophage; toxin of the YkfI-YafW toxin-antitoxin system	50	82
b0246	264007	263690	<i>yafW</i>	CP4-6 prophage; antitoxin of the YkfI-YafW toxin-antitoxin system	32	54
b0247	264732	264256	<i>ykfG</i>	CP4-6 prophage; RadC-like JAB domain protein	19	63
b0248	265206	264748	<i>yafX</i>	CP4-6 prophage; uncharacterized protein	211	345
b0249	265543	265304	<i>ykfF</i>	CP4-6 prophage; uncharacterized protein	24	28
b0250	266087	265620	<i>ykfB</i>	CP4-6 prophage; uncharacterized protein	911	634
b0251	266553	266110	<i>yafY</i>	lipoprotein, inner membrane; degP regulator; CP4-6 prophage	81	77
b0252	268005	267184	<i>yafZ</i>	CP4-6 prophage; conserved protein	45	458
b0253	268960	268097	<i>ykfA</i>	CP4-6 prophage; putative GTP-binding protein	146	278
b0254	270182	269289	<i>perR</i>	CP4-6 prophage; putative DNA-binding transcriptional regulator	170	886
b0256	270603	271754	<i>insI1</i>	IS30 transposase	353	1322
b0259	275117	274101	<i>insH1</i>	IS5 transposase and trans-activator	3143	2558
b0260	275325	276728	<i>mmuP</i>	CP4-6 prophage; putative S-methylmethionine transporter	336	1884
b0261	276715	277647	<i>mmuM</i>	CP4-6 prophage; S-methylmethionine:homocysteine methyltransferase	1243	933
b0262	278802	277756	<i>afuC</i>	CP4-6 prophage; putative ferric transporter subunit	26	90
b0264	279681	279178	<i>insB1</i>	IS1 transposase B	84	241
b0265	279875	279600	<i>insA</i>	IS1 repressor TnpA	27	166
b0267	281983	280829	<i>yagA</i>	CP4-6 prophage; putative DNA-binding transcriptional regulator	4	303
b0268	282278	283186	<i>yagE</i>	2-keto-3-deoxy gluconate (KDG) aldolase; CP4-6 prophage	821	45
b0269	283201	285168	<i>yagF</i>	CP4-6 prophage; dehydratase family protein	731	84
b0270	285395	286777	<i>yagG</i>	CP4-6 prophage; putative sugar transporter	89	60
b0271	286789	288399	<i>yagH</i>	CP4-6 prophage; putative xylosidase/arabinosidase	103	78
b0272	289162	288404	<i>yagI</i>	CP4-6 prophage; putative DNA-binding transcriptional regulator	120	499
b0273	290305	289301	<i>argF</i>	ornithine carbamoyltransferase 2, chain F; CP4-6 prophage	57	3530
b0274	291152	290649	<i>insB1</i>	IS1 transposase B	84	241
b0275	291346	291071	<i>insA</i>	IS1 repressor TnpA	27	166
b0277	292948	292322	<i>yagK</i>	CP4-6 prophage; conserved protein	195	744
b0278	293918	293220	<i>yagL</i>	CP4-6 prophage; DNA-binding protein	281	708
b0279	294799	293945	<i>yagM</i>	CP4-6 prophage; uncharacterized protein	70	280
b0280	295579	295139	<i>yagN</i>	CP4-6 prophage; uncharacterized protein	1113	2515
b0281	297096	295696	<i>intF</i>	CP4-6 prophage; putative phage integrase	1031	3644
b0283	298726	297770	<i>paoD</i>	moco insertion factor for PaoABC aldehyde oxidoreductase	50	53
b0284	300934	298736	<i>paoC</i>	PaoABC aldehyde oxidoreductase, Moco-containing subunit	98	175
b0285	301887	300931	<i>paoB</i>	PaoABC aldehyde oxidoreductase, FAD-containing subunit	51	105
b0286	302573	301884	<i>paoA</i>	PaoABC aldehyde oxidoreductase, 2Fe-2S subunit	46	98
b0287	302991	303605	<i>yagU</i>	DUF1440 family inner membrane acid resistance protein	2713	289
b0288	304182	303853	<i>ykgJ</i>	UPF0153 cysteine cluster protein	92	171
b0289	305205	304495	<i>ecpE</i>	ECP production pilus chaperone	90	129
b0290	306817	305174	<i>ecpD</i>	polymerized tip adhesin of ECP fibers	269	540
b0291	309332	306807	<i>ecpC</i>	ECP production outer membrane protein	107	232
b0292	310026	309358	<i>ecpB</i>	ECP production pilus chaperone	18	25
b0293	310671	310084	<i>ecpA</i>	ECP pilin	159	153
b0294	311336	310746	<i>ecpR</i>	putative transcriptional regulator for the ecp operon	13	447
b0295	312112	312339	<i>ykgL</i>	uncharacterized protein	166	232
b0296	312777	312514	<i>ykgM</i>	50S ribosomal protein L31 type B; alternative zinc-	141	86

				limitation L31 protein		
b0298	315291	315590	<i>insE1</i>	IS3 transposase A	106	309
b0299	315587	316453	<i>insF1</i>	IS3 transposase B	106	239
b0301	318319	317726	<i>rclC</i>	reactive chlorine species (RCS) stress resistance inner membrane protein	63	168
b0303	318567	318331	<i>rclB</i>	reactive chlorine species (RCS) stress resistance periplasmic protein	21	42
b0304	320001	318676	<i>rclA</i>	reactive chlorine stress species (RCS) resistance protein; pyridine nucleotide-dependent disulfide oxidoreductase family	514	321
b0305	320227	321081	<i>rclR</i>	reactive chlorine species (RCS)-specific activator of the rcl genes	346	112
b0306	321608	322327	<i>ykgE</i>	cysteine-rich LutA family protein; putative electron transport chain YkgEFG component	1539	205
b0307	322338	323765	<i>ykgF</i>	ferridoxin-like LutB family protein; putative electron transport chain YkgEFG component	2462	434
b0308	323758	324453	<i>ykgG</i>	LutC family protein; putative electron transport chain YkgEFG component	940	250
b0310	325364	324696	<i>ykgH</i>	putative inner membrane protein	14	186
b0311	327247	325577	<i>betA</i>	choline dehydrogenase, a flavoprotein	319	590
b0312	328733	327261	<i>betB</i>	betaine aldehyde dehydrogenase, NAD-dependent	346	747
b0313	329334	328747	<i>betI</i>	choline-inducible betIBA-betT divergent operon transcriptional repressor	204	926
b0314	329463	331496	<i>betT</i>	choline transporter of high affinity	324	1073
b0315	332371	333459	<i>yahA</i>	c-di-GMP-specific phosphodiesterase	355	684
b0316	334433	333501	<i>yahB</i>	putative DNA-binding transcriptional regulator	464	522
b0317	335022	334525	<i>yahC</i>	putative inner membrane protein	120	154
b0318	335280	335885	<i>yahD</i>	ankyrin repeat protein	250	226
b0319	335925	336788	<i>yahE</i>	DUF2877 family protein	29	76
b0320	336778	338325	<i>yahF</i>	putative NAD(P)-binding succinyl-CoA synthase	36	162
b0321	338325	339743	<i>yahG</i>	DUF1116 family protein	36	35
b0323	340165	341115	<i>yahI</i>	carbamate kinase-like protein	15	26
b0324	341125	342507	<i>yahJ</i>	putative metallo-dependent hydrolase domain deaminase	484	258
b0325	342884	343933	<i>yahK</i>	broad specificity NADPH-dependent aldehyde reductase, Zn-containing	858	688
b0326	344176	344991	<i>yahL</i>	uncharacterized protein	14	221
b0327	345404	345649	<i>yahM</i>	uncharacterized protein	182	205
b0328	346337	345666	<i>yahN</i>	amino acid exporter for proline, lysine, glutamate, homoserine	1716	595
b0329	346484	346759	<i>yahO</i>	periplasmic protein, function unknown, YhcN family	4103	5626
b0330	348443	346857	<i>prpR</i>	propionate catabolism operon regulatory protein	914	510
b0331	348682	349572	<i>prpB</i>	2-methylisocitrate lyase	16	262
b0333	350012	351181	<i>prpC</i>	2-methylcitrate synthase	23	252
b0334	351215	352666	<i>prpD</i>	2-methylcitrate dehydratase	22	326
b0335	352706	354592	<i>prpE</i>	propionate--CoA ligase	37	348
b0336	354922	356181	<i>codB</i>	cytosine transporter	462	645
b0337	356171	357454	<i>codA</i>	cytosine/isoguanine deaminase	1485	726
b0338	358690	357791	<i>cynR</i>	transcriptional activator of cyn operon; autorepressor	86	85
b0339	358799	359458	<i>cynT</i>	carbonic anhydrase	36	42
b0340	359489	359959	<i>cynS</i>	cyanate aminohydrolase	31	52
b0341	359992	361146	<i>cynX</i>	putative cyanate transporter	21	94
b0342	361860	361249	<i>lacA</i>	thiogalactoside acetyltransferase	89	126
b0343	363179	361926	<i>lacY</i>	lactose permease	178	588
b0344	366305	363231	<i>lacZ</i>	beta-D-galactosidase	993	171
b0345	367510	366428	<i>lacI</i>	lactose-inducible lac operon transcriptional repressor	1577	609
b0346	368420	367587	<i>mhpR</i>	mhp operon transcriptional activator	7231	767
b0347	368611	370275	<i>mhpA</i>	3-(3-hydroxyphenyl)propionate hydroxylase	30	43

b0348	370277	371221	<i>mhpB</i>	2,3-dihydroxyphenylpropionate 1,2-dioxygenase	19	22
b0349	371239	372105	<i>mhpC</i>	2-hydroxy-6-ketono-2,4-dienedioic acid hydrolase	46	122
b0350	372115	372924	<i>mhpD</i>	2-keto-4-pentenoate hydratase	44	39
b0351	372921	373871	<i>mhpF</i>	acetaldehyde-CoA dehydrogenase II, NAD-binding	52	39
b0352	373868	374881	<i>mhpE</i>	4-hydroxy-2-oxovalerate/4-hydroxy-2-oxopentanoic acid aldolase, class I	39	43
b0353	375459	376670	<i>mhpT</i>	3-hydroxyphenylpropionic transporter	38	81
b0354	376772	377311	<i>yaiL</i>	DUF2058 family protein	608	690
b0355	378368	377535	<i>frmB</i>	S-formylglutathione hydrolase	905	1046
b0356	379571	378462	<i>frmA</i>	alcohol dehydrogenase class III; glutathione-dependent formaldehyde dehydrogenase	2037	1233
b0357	379881	379606	<i>frmR</i>	regulator protein that represses frmRAB operon	274	290
b0358	380842	380069	<i>yaiO</i>	outer membrane protein	61	212
b0360	381351	381716	<i>insC1</i>	IS2 repressor TnpA	403	429
b0361	381674	382579	<i>insD1</i>	IS2 transposase TnpB	652	819
b0363	383935	382739	<i>yaiP</i>	putative family 2 glycosyltransferase	80	658
b0364	384616	384059	<i>yaiS</i>	putative PIG-L family deacetylase	7	86
b0365	385232	386194	<i>tauA</i>	taurine ABC transporter periplasmic binding protein	122	51
b0366	386207	386974	<i>tauB</i>	taurine ABC transporter ATPase	59	45
b0367	386971	387798	<i>tauC</i>	taurine ABC transporter permease	30	39
b0368	387795	388646	<i>tauD</i>	taurine dioxygenase, 2-oxoglutarate-dependent	119	85
b0369	389727	388753	<i>hemB</i>	5-aminolevulinate dehydratase (prophobilinogen synthase)	5027	1198
b0372	392605	391739	<i>insF1</i>	IS3 transposase B	106	239
b0373	392901	392602	<i>insE1</i>	IS3 transposase A	106	309
b0375	394506	395129	<i>yaiV</i>	putative transcriptional regulator	46	297
b0376	396287	395130	<i>ampH</i>	D-alanyl-D-alanine- carboxypeptidase/endopeptidase; penicillin-binding protein; weak beta-lactamase	903	501
b0377	396639	397859	<i>sbmA</i>	peptide antibiotic transporter	568	1630
b0378	397872	398966	<i>yaiW</i>	microcin Bac7 uptake protein; outer membrane surface-exposed lipoprotein	790	1144
b0379	399333	399025	<i>yaiY</i>	DUF2755 family inner membrane protein	753	404
b0380	399593	399805	<i>yaiZ</i>	DUF2754 family putative inner membrane protein	517	383
b0381	400923	399829	<i>ddlA</i>	D-alanine-D-alanine ligase A	2968	1420
b0382	401386	401646	<i>iraP</i>	anti-RssB factor, RpoS stabilizer during Pi starvation; anti-adaptor protein	2293	1737
b0383	401747	403162	<i>phoA</i>	bacterial alkaline phosphatase	9540	904
b0384	403281	403601	<i>psiF</i>	PsiF family protein	2131	1492
b0385	403703	404818	<i>yaiC</i>	diguanylate cyclase, cellulose regulator	58	280
b0386	405644	404835	<i>proC</i>	pyrroline-5-carboxylate reductase, NAD(P)-binding	1490	1201
b0387	405764	406222	<i>yaiI</i>	UPF0178 family protein	382	306
b0388	406405	406929	<i>aroL</i>	shikimate kinase II	493	1709
b0389	406979	407170	<i>yaiA</i>	OxyR-regulated conserved protein	830	2215
b0390	407428	408105	<i>aroM</i>	AroM family protein	172	458
b0391	408177	408461	<i>yaiE</i>	UPF0345 family protein	1483	1155
b0393	410019	409108	<i>rdgC</i>	nucleoid-associated ssDNA and dsDNA binding protein; competitive inhibitor of RecA function	1390	1152
b0394	410144	411052	<i>mak</i>	manno(fructo)kinase	1225	218
b0396	412481	411297	<i>araJ</i>	L-arabinose-inducible putative transporter, MFS family	143	386
b0397	415753	412607	<i>sbcC</i>	exonuclease, dsDNA, ATP-dependent	1169	1104
b0398	416952	415750	<i>sbcD</i>	exonuclease, dsDNA, ATP-dependent	465	352
b0399	417142	417831	<i>phoB</i>	response regulator in two-component regulatory system with PhoR	716	1546
b0400	417889	419184	<i>phoR</i>	sensory histidine kinase in two-component regulatory system with PhoB	356	1576
b0401	419591	420910	<i>brnQ</i>	branched-chain amino acid transport system 2 carrier protein; LIV-II transport system for Ile, Leu, and Val	739	714

b0402	420986	422359	<i>proY</i>	proline-specific permease	515	433
b0403	422518	424332	<i>malZ</i>	maltodextrin glucosidase	754	862
b0404	424918	424337	<i>acpH</i>	acyl carrier protein (ACP) phosphodiesterase; ACP hydrolyase	269	201
b0405	425011	426081	<i>queA</i>	S-adenosylmethionine:tRNA ribosyltransferase-isomerase	359	349
b0406	426137	427264	<i>tgt</i>	tRNA-guanine transglycosylase	2633	3166
b0407	427287	427619	<i>yajC</i>	SecYEG protein translocase auxillary subunit	3335	3220
b0408	427647	429494	<i>secD</i>	SecYEG protein translocase auxillary subunit	4542	3934
b0409	429505	430476	<i>secF</i>	SecYEG protein translocase auxillary subunit	3195	2129
b0410	430605	430952	<i>yajD</i>	HNH nuclease family protein	961	2627
b0411	432013	431129	<i>tsx</i>	nucleoside channel, receptor of phage T6 and colicin K	28021	2408
b0412	432851	432312	<i>yajI</i>	putative lipoprotein	970	527
b0413	433002	433451	<i>nrdR</i>	Nrd regulon repressor	940	415
b0414	433455	434558	<i>ribD</i>	fused diaminohydroxyphosphoribosylaminopyrimidine deaminase and 5-amino-6-(5-phosphoribosylamino) uracil reductase	1240	721
b0415	434647	435117	<i>ribE</i>	riboflavin synthase beta chain	817	325
b0416	435137	435556	<i>nusB</i>	transcription antitermination protein	1866	685
b0417	435634	436611	<i>thiL</i>	thiamine monophosphate kinase	550	456
b0418	436589	437107	<i>pgpA</i>	phosphatidylglycerophosphatase A	611	1185
b0419	438135	437161	<i>yajO</i>	2-carboxybenzaldehyde reductase	4202	1424
b0420	440177	438315	<i>dxs</i>	1-deoxyxylulose-5-phosphate synthase, thiamine triphosphate-binding, FAD-requiring	3267	1598
b0421	441101	440202	<i>ispA</i>	geranyltranstransferase	1469	724
b0422	441343	441101	<i>xseB</i>	exonuclease VII small subunit	1307	1224
b0423	441549	442997	<i>thiI</i>	tRNA s(4)U8 sulfurtransferase	1175	734
b0424	443641	443051	<i>yajL</i>	oxidative-stress-resistance chaperone	518	218
b0425	444515	443604	<i>panE</i>	2-dehydropanoate reductase, NADPH-specific	1105	772
b0426	444683	445174	<i>yajQ</i>	phage Phi6 host factor, ATP/GTP binding protein	7634	4416
b0427	446666	445302	<i>yajR</i>	putative transporter	460	487
b0428	447705	446815	<i>cyoE</i>	protoheme IX farnesyltransferase	12637	4053
b0429	448046	447717	<i>cyoD</i>	cytochrome o ubiquinol oxidase subunit IV	4095	677
b0430	448660	448046	<i>cyoC</i>	cytochrome o ubiquinol oxidase subunit III	10501	2172
b0431	450641	448650	<i>cyoB</i>	cytochrome o ubiquinol oxidase subunit I	38268	5785
b0432	451610	450663	<i>cyoA</i>	cytochrome o ubiquinol oxidase subunit II	38317	7253
b0433	453545	452070	<i>ampG</i>	muropeptide transporter	499	498
b0434	454167	453589	<i>yajG</i>	putative lipoprotein	3076	1968
b0435	454472	454789	<i>bolA</i>	stationary-phase morphogene, transcriptional repressor for mreB; also regulator for dacA, dacC, and ampC	12069	11727
b0436	455133	456431	<i>tig</i>	peptidyl-prolyl cis/trans isomerase (trigger factor)	33496	9855
b0437	456677	457300	<i>clpP</i>	proteolytic subunit of ClpA-ClpP and ClpX-ClpP ATP-dependent serine proteases	9179	3752
b0438	457426	458700	<i>clpX</i>	ATPase and specificity subunit of ClpX-ClpP ATP-dependent serine protease	11009	5863
b0439	458888	461242	<i>lon</i>	DNA-binding ATP-dependent protease La	22012	6595
b0440	461451	461723	<i>hupB</i>	HU, DNA-binding transcriptional regulator, beta subunit	13565	6061
b0441	461915	463786	<i>ppiD</i>	periplasmic folding chaperone, has an inactive PPIase domain	6992	4043
b0442	463937	464308	<i>ybaV</i>	putative competence-suppressing periplasmic helix-hairpin-helix DNA-binding protein	312	321
b0443	464402	464800	<i>fadM</i>	long-chain acyl-CoA thioesterase III	374	2182
b0444	465547	464852	<i>queC</i>	7-cyano-7-deazaguanine (preQ0) synthase; queuosine biosynthesis	1102	689
b0445	467312	465612	<i>ybaE</i>	putative ABC transporter periplasmic binding protein	2380	571
b0446	467412	468230	<i>cof</i>	thiamine pyrimidine pyrophosphate hydrolase; HMP-PP phosphatase	402	1186
b0447	468383	468841	<i>ybaO</i>	putative DNA-binding transcriptional regulator	1317	1398

b0448	468871	470643	<i>mdlA</i>	putative multidrug ABC transporter ATPase	1390	843
b0449	470636	472417	<i>mdlB</i>	putative multidrug ABC transporter ATPase	989	568
b0450	472598	472936	<i>glnK</i>	nitrogen assimilation regulatory protein for GlnL, GlnE, and AmtB	9	25
b0451	472966	474252	<i>amtB</i>	ammonium transporter	85	251
b0452	475161	474301	<i>tesB</i>	acyl-CoA thioesterase 2	1296	727
b0453	475379	475951	<i>ybaY</i>	outer membrane lipoprotein	2311	2576
b0454	476371	475982	<i>ybaZ</i>	excision repair protein, alkyltransferase-like protein ATL	81	214
b0456	476672	477025	<i>ybaA</i>	DUF1428 family protein	33	378
b0457	478617	477067	<i>ylaB</i>	putative membrane-anchored cyclic-di-GMP phosphodiesterase	919	1267
b0458	479251	478781	<i>ylaC</i>	DUF1449 family inner membrane protein	860	1240
b0459	479918	479367	<i>maa</i>	maltose O-acetyltransferase	466	2395
b0460	480308	480090	<i>hha</i>	modulator of gene expression, with H-NS	1616	11686
b0461	480708	480334	<i>tomB</i>	Hha toxicity attenuator; conjugation-related protein	1443	21083
b0462	484403	481254	<i>acrB</i>	multidrug efflux system protein	1788	1895
b0463	485619	484426	<i>acrA</i>	multidrug efflux system	3620	1994
b0464	485761	486408	<i>acrR</i>	transcriptional repressor	380	1897
b0465	486536	489898	<i>mscK</i>	mechanosensitive channel protein, intermediate conductance, K ⁺ regulated	1536	2465
b0466	490271	490110	<i>ybaM</i>	DUF2496 family protein	24	70
b0467	490812	490285	<i>priC</i>	primosomal replication protein N"	108	108
b0468	490882	491259	<i>ybaN</i>	DUF454 family inner membrane protein	206	151
b0469	491412	491963	<i>apt</i>	adenine phosphoribosyltransferase	1060	477
b0470	492092	494023	<i>dnaX</i>	DNA polymerase III/DNA elongation factor III, tau and gamma subunits	838	992
b0471	494076	494405	<i>ybaB</i>	DNA-binding protein, putative nucleoid-associated protein	3342	871
b0472	494405	495010	<i>recR</i>	gap repair protein	2210	494
b0473	495120	496994	<i>htpG</i>	protein refolding molecular co-chaperone Hsp90, Hsp70-dependent; heat-shock protein; ATPase	30324	11638
b0474	497175	497819	<i>adk</i>	adenylate kinase	10283	5240
b0475	498055	499017	<i>hemH</i>	ferrochelataase	509	404
b0476	499973	499014	<i>aes</i>	acetyl esterase	870	345
b0477	500125	501429	<i>gsk</i>	inosine/guanosine kinase	643	688
b0478	503238	501562	<i>ybaL</i>	inner membrane putative NAD(P)-binding transporter	1102	1249
b0479	504696	503476	<i>fsr</i>	putative fosmidomycin efflux system protein	301	412
b0480	504914	506566	<i>ushA</i>	bifunctional UDP-sugar hydrolase/5'-nucleotidase	8128	1351
b0481	507082	506603	<i>ybaK</i>	Cys-tRNA(Pro)/Cys-tRNA(Cys) deacylase	558	167
b0482	508080	507286	<i>ybaP</i>	TraB family protein	391	388
b0483	508218	508559	<i>ybaQ</i>	putative DNA-binding transcriptional regulator	309	1209
b0484	511379	508875	<i>copA</i>	copper transporter	1104	5449
b0485	511641	512573	<i>glsA</i>	glutaminase 1	45	91
b0486	512576	513868	<i>ybaT</i>	putative amino acid transporter	55	250
b0487	513993	514400	<i>cueR</i>	copper-responsive regulon transcriptional regulator	405	384
b0488	514859	514401	<i>ybbJ</i>	inner membrane protein; stimulator of the QmcA suppressor of ftsH-htpX	384	263
b0489	515773	514856	<i>qmcA</i>	PHB domain membrane-anchored putative protease	2461	2027
b0490	515919	516596	<i>fetA</i>	iron export ABC transporter ATPase; peroxide resistance protein	731	875
b0491	516583	517362	<i>fetB</i>	iron export ABC transporter permease; peroxide resistance protein	312	291
b0492	518279	517425	<i>ybbN</i>	DnaK co-chaperone, thioredoxin-like protein	3367	2224
b0493	519149	518340	<i>ybbO</i>	putative oxidoreductase	403	425
b0494	519765	519139	<i>tesA</i>	acyl-CoA thioesterase 1 and protease I and lysophospholipase L1	316	1423
b0495	519733	520419	<i>ybbA</i>	putative ABC transporter ATPase	153	294

b0496	520416	522830	<i>ybbP</i>	putative ABC transporter permease	187	462
b0497	523261	527541	<i>rhsD</i>	Rhs protein with DUF4329 family putative toxin domain; putative neighboring cell growth inhibitor	241	1942
b0498	527581	527949	<i>ybbC</i>	putative immunity protein	96	618
b0503	531226	530132	<i>mmhH</i>	tRNA 2-selenouridine synthase, selenophosphate-dependent	314	209
b0504	532221	531295	<i>allS</i>	allD operon transcriptional activator	102	97
b0505	532451	532933	<i>allA</i>	ureidoglycolate lyase, releasing urea	74	78
b0506	533011	533826	<i>allR</i>	glyoxylate-inducible transcriptional repressor of all and gcl operons	1582	1231
b0507	533916	535697	<i>gcl</i>	glyoxylate carboligase	70	207
b0508	535710	536486	<i>hyi</i>	hydroxypyruvate isomerase	19	123
b0509	536586	537464	<i>glxR</i>	tartronate semialdehyde reductase, NADH-dependent	23	110
b0511	537633	539087	<i>ybbW</i>	putative allantoin transporter	11	238
b0512	539147	540508	<i>allB</i>	allantoinase	79	159
b0513	540565	541866	<i>ybbY</i>	putative uracil/xanthine transporter	45	145
b0514	541888	543033	<i>glxK</i>	glycerate kinase II	153	122
b0515	544046	543261	<i>allE</i>	S-ureidoglycine aminohydrolase	653	423
b0516	545292	544057	<i>allC</i>	allantoate amidohydrolase	187	267
b0517	546363	545314	<i>allD</i>	ureidoglycolate dehydrogenase	93	83
b0518	546680	548347	<i>fdrA</i>	putative NAD(P)-binding acyl-CoA synthetase	13	39
b0520	549627	550442	<i>ylbF</i>	putative anaerobic allantoin catabolic oxamate carbamoyltransferase; DUF2877 family protein	8	43
b0521	550439	551332	<i>ybcF</i>	putative carbonate kinase	23	117
b0522	552594	551527	<i>purK</i>	N5-carboxyaminoimidazole ribonucleotide synthase	255	285
b0523	553100	552591	<i>purE</i>	N5-carboxyaminoimidazole ribonucleotide mutase	90	63
b0524	553940	553218	<i>lpxH</i>	UDP-2,3-diacylglucosamine pyrophosphohydrolase	389	136
b0525	554437	553943	<i>ppiB</i>	peptidyl-prolyl cis-trans isomerase B (rotamase B)	9766	5208
b0526	554611	555996	<i>cysS</i>	cysteinyl-tRNA synthetase	1885	1144
b0527	556553	556032	<i>ybcI</i>	DUF457 family inner membrane protein	30	206
b0528	556873	556661	<i>ybcJ</i>	ribosome-associated protein; putative RNA-binding protein	85	34
b0529	557741	556875	<i>folD</i>	bifunctional 5,10-methylene-tetrahydrofolate dehydrogenase/ 5,10-methylene-tetrahydrofolate cyclohydrolase	1636	510
b0530	558212	558754	<i>sfnA</i>	FimA homolog, function unknown	57	57
b0531	558974	559666	<i>sfnC</i>	putative periplasmic pilus chaperone	11	106
b0532	559697	562300	<i>sfnD</i>	putative outer membrane export usher protein	31	474
b0533	562336	563319	<i>sfnH</i>	FimA homolog, function unknown	5	116
b0534	563330	563845	<i>sfnF</i>	FimA homolog, function unknown	7	36
b0535	564480	563848	<i>sfnZ</i>	response regulator family protein	12	95
b0537	565978	564815	<i>intD</i>	DLP12 prophage; putative phage integrase	1060	2530
b0540	566842	567141	<i>insE1</i>	IS3 transposase A	106	309
b0541	567138	568004	<i>insF1</i>	IS3 transposase B	106	239
b0543	568315	568647	<i>emrE</i>	DLP12 prophage; multidrug resistance protein	152	270
b0544	568902	570428	<i>ybcK</i>	DLP12 prophage; putative recombinase	45	678
b0545	570893	571444	<i>ybcL</i>	inactive polymorphonuclear leukocyte migration suppressor; DLP12 prophage; UPF0098 family secreted protein	81	899
b0546	571454	572251	<i>ybcM</i>	DLP12 prophage; putative DNA-binding transcriptional regulator	410	3307
b0547	572466	572921	<i>ybcN</i>	DLP12 prophage; uncharacterized protein	6	20
b0548	572921	573091	<i>ninE</i>	DLP12 prophage; conserved protein	1	12
b0549	573084	573374	<i>ybcO</i>	DLP12 prophage; uncharacterized protein	5	32
b0550	573371	573733	<i>rusA</i>	DLP12 prophage; endonuclease RUS	2	10
b0551	573956	574339	<i>quuD</i>	DLP12 prophage; putative antitermination protein	12	156
b0552	575753	574737	<i>insH1</i>	IS5 transposase and trans-activator	3143	2558

b0554	577398	577613	<i>essD</i>	DLP12 prophage; putative phage lysis protein	6	62
b0555	577613	578110	<i>rrrD</i>	DLP12 prophage; putative lysozyme	33	294
b0556	578107	578568	<i>rzpD</i>	DLP12 prophage; putative murein endopeptidase	82	125
b0557	578893	578600	<i>borD</i>	DLP12 prophage; putative lipoprotein	723	1463
b0558	579594	579184	<i>ybcV</i>	DLP12 prophage; uncharacterized protein	8	540
b0559	579880	580086	<i>ybcW</i>	DLP12 prophage; uncharacterized protein	8	147
b0560	580834	581379	<i>nohD</i>	DLP12 prophage; DNA packaging protein	44	188
b0564	583681	584430	<i>appY</i>	global transcriptional activator; DLP12 prophage	1331	1478
b0565	585633	584680	<i>ompT</i>	DLP12 prophage; outer membrane protease VII; outer membrane protein 3b	24800	20212
b0566	586908	586147	<i>envY</i>	porin thermoregulatory transcriptional activator	60	222
b0567	587981	587091	<i>ybcH</i>	PRK09936 family protein	97	159
b0568	590954	587982	<i>nfrA</i>	bacteriophage N4 receptor, outer membrane subunit	362	558
b0569	593178	590941	<i>nfrB</i>	bacteriophage N4 receptor, inner membrane subunit	211	546
b0570	594770	593328	<i>cusS</i>	copper-sensing histidine kinase in two-component regulatory system with CusR	225	476
b0571	595443	594760	<i>cusR</i>	response regulator in two-component regulatory system with CusS	118	221
b0572	595600	596973	<i>cusC</i>	copper/silver efflux system, outer membrane component	23	65
b0573	597131	597463	<i>cusF</i>	periplasmic copper- and silver-binding protein	22	36
b0574	597479	598702	<i>cusB</i>	copper/silver efflux system, membrane fusion protein	28	58
b0575	598714	601857	<i>cusA</i>	copper/silver efflux system, membrane component	45	277
b0576	601959	603335	<i>pheP</i>	phenylalanine transporter	233	417
b0577	604663	603416	<i>ybdG</i>	mechanosensitive channel protein, miniconductance	827	678
b0578	605424	604771	<i>nfsB</i>	dihydropteridine reductase, NAD(P)H-dependent, oxygen-insensitive	2999	854
b0579	605886	605518	<i>ybdF</i>	DUF419 family protein	349	455
b0580	606199	605951	<i>ybdJ</i>	DUF1158 family putative inner membrane protein	98	128
b0581	607383	606265	<i>ybdK</i>	weak gamma-glutamyl:cysteine ligase	1724	1200
b0582	608065	609177	<i>insLI</i>	IS186 transposase	756	842
b0583	610079	609459	<i>entD</i>	phosphopantetheinyltransferase component of enterobactin synthase multienzyme complex	53	175
b0584	612494	610254	<i>fepA</i>	ferrienterobactin outer membrane transporter	1901	852
b0585	612737	613939	<i>fes</i>	enterobactin/ferrienterobactin esterase	423	266
b0586	614157	618038	<i>entF</i>	enterobactin synthase multienzyme complex component, ATP-dependent	1914	465
b0587	618254	619387	<i>fepE</i>	regulator of length of O-antigen component of lipopolysaccharide chains	22	118
b0588	620199	619384	<i>fepC</i>	ferrienterobactin ABC transporter ATPase	405	124
b0589	621188	620196	<i>fepG</i>	iron-enterobactin ABC transporter permease	100	41
b0590	622189	621185	<i>fepD</i>	ferrienterobactin ABC transporter permease	211	154
b0591	622300	623550	<i>entS</i>	enterobactin exporter, iron-regulated	256	175
b0592	624510	623554	<i>fepB</i>	ferrienterobactin ABC transporter periplasmic binding protein	423	234
b0593	624885	626060	<i>entC</i>	isochorismate synthase 1	1752	293
b0594	626070	627680	<i>entE</i>	2,3-dihydroxybenzoate-AMP ligase component of enterobactin synthase multienzyme complex	1949	367
b0595	627694	628551	<i>entB</i>	isochorismatase	1780	257
b0596	628551	629297	<i>entA</i>	2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase	733	154
b0597	629300	629713	<i>entH</i>	enterobactin synthesis proofreading thioesterase	327	87
b0598	629894	631999	<i>cstA</i>	carbon starvation protein involved in peptide utilization; APC peptide transporter family protein	7649	3811
b0599	633477	632389	<i>ybdH</i>	putative oxidoreductase	540	1980
b0600	633586	634746	<i>ybdL</i>	methionine aminotransferase, PLP-dependent	800	3498
b0601	635376	634747	<i>ybdM</i>	Spo0J family protein, ParB-like nuclease domain	212	385
b0602	636569	635349	<i>ybdN</i>	PAPS reductase-like domain protein	44	211
b0603	637618	636716	<i>ybdO</i>	putative DNA-binding transcriptional regulator	42	435

b0604	638573	637827	<i>dsbG</i>	thiol:disulfide interchange protein, periplasmic	1388	1747
b0605	638945	639508	<i>ahpC</i>	alkyl hydroperoxide reductase, C22 subunit	19404	11049
b0606	639753	641318	<i>ahpF</i>	alkyl hydroperoxide reductase, F52a subunit, FAD/NAD(P)-binding	4792	1721
b0607	641867	641439	<i>uspG</i>	universal stress protein UP12	5885	4232
b0608	642088	643326	<i>ybdR</i>	putative Zn-dependent NAD(P)-binding oxidoreductase	141	779
b0610	643967	643557	<i>rnk</i>	regulator of nucleoside diphosphate kinase	1585	589
b0611	645003	644197	<i>rna</i>	ribonuclease I	1387	1447
b0612	646580	645117	<i>citT</i>	citrate/succinate antiporter; citrate carrier	62	379
b0613	647509	646631	<i>citG</i>	2-(5"-triphosphoribosyl)-3'-dephosphocoenzyme-A synthase	8	27
b0614	648035	647484	<i>citX</i>	apo-citrate lyase phosphoribosyl-dephospho-CoA transferase	42	21
b0615	649571	648039	<i>citF</i>	citrate lyase, citrate-ACP transferase (alpha) subunit	37	24
b0616	650490	649582	<i>citE</i>	citrate lyase, citryl-ACP lyase (beta) subunit	33	31
b0617	650783	650487	<i>citD</i>	citrate lyase, acyl carrier (gamma) subunit	4	5
b0618	651856	650798	<i>citC</i>	citrate lyase ligase; [citrate [pro-3S]-lyase] ligase	56	1247
b0619	652235	653893	<i>citA</i>	sensory histidine kinase in two-component regulatory system with CitB	158	479
b0620	653862	654542	<i>citB</i>	response regulator in two-component regulatory system with CitA	389	229
b0621	655968	654583	<i>dcuC</i>	anaerobic C4-dicarboxylate transport	11574	927
b0622	656557	657117	<i>pagP</i>	phospholipid:lipid A palmitoyltransferase	901	771
b0623	657292	657501	<i>cspE</i>	constitutive cold shock family transcription antitermination protein; negative regulator of cspA transcription; RNA melting protein; ssDNA-binding protein	92661	133624
b0624	657938	657555	<i>flc</i>	fluoride efflux channel, dual topology membrane protein	345	888
b0627	658947	659150	<i>tatE</i>	TatABCE protein translocation system subunit	1628	1909
b0628	660216	659251	<i>lipA</i>	lipoate synthase	10592	2292
b0629	661378	660425	<i>ybeF</i>	LysR family putative transcriptional regulator	89	507
b0630	662278	661637	<i>lipB</i>	octanoyltransferase; octanoyl-[ACP]:protein N-octanoyltransferase	733	882
b0631	662642	662379	<i>ybeD</i>	UPF0250 family protein	3457	6798
b0632	663963	662752	<i>dacA</i>	D-alanyl-D-alanine carboxypeptidase (penicillin-binding protein 5)	3769	2095
b0633	665190	664102	<i>rlpA</i>	septal ring protein, suppressor of prc, minor lipoprotein	3289	2260
b0634	666313	665201	<i>mrdB</i>	cell wall shape-determining protein	846	591
b0635	668217	666316	<i>mrdA</i>	penicillin-binding protein 2, transpeptidase involved in peptidoglycan synthesis	894	1282
b0636	668715	668248	<i>rlmH</i>	23S rRNA m(3)Psi1915 pseudouridine methyltransferase, SAM-dependent	405	245
b0637	669036	668719	<i>rsfS</i>	ribosomal silencing factor	393	394
b0638	669907	669296	<i>cobC</i>	putative alpha-ribazole-5'-P phosphatase	155	153
b0639	670572	669931	<i>nadD</i>	nicotinic acid mononucleotide adenyltransferase, NAD(P)-dependent	704	685
b0640	671605	670574	<i>holA</i>	DNA polymerase III, delta subunit	985	1633
b0641	672186	671605	<i>lptE</i>	LPS assembly OM complex LptDE, lipoprotein component	4033	1433
b0642	674783	672201	<i>leuS</i>	leucyl-tRNA synthetase	11988	6047
b0643	675018	675500	<i>ybeL</i>	DUF1451 family protein	22361	6467
b0644	676547	675570	<i>ybeQ</i>	Sel1 family TPR-like repeat protein	240	351
b0645	676711	677418	<i>ybeR</i>	uncharacterized protein	4	183
b0646	677415	678842	<i>djlB</i>	putative HscC co-chaperone, uncharacterized J domain-containing protein	22	421
b0647	679406	678852	<i>ybeT</i>	Sel1 family TPR-like repeat protein	4	69
b0648	679508	680215	<i>ybeU</i>	DUF1266 family protein	19	341
b0649	680212	681663	<i>djlC</i>	J domain-containing HscC co-chaperone; Hsc56	64	739
b0650	683393	681723	<i>hscC</i>	Hsp70 family chaperone Hsc62; RpoD-binding	173	234

				transcription inhibitor		
b0651	684412	683477	<i>rihA</i>	ribonucleoside hydrolase 1	10184	1660
b0652	685255	684530	<i>gltL</i>	glutamate/aspartate ABC transporter ATPase	1737	806
b0653	685929	685255	<i>gltK</i>	glutamate/aspartate ABC transporter permease	458	407
b0654	686669	685929	<i>gltJ</i>	glutamate/aspartate ABC transporter permease	369	227
b0655	687747	686839	<i>gltI</i>	glutamate/aspartate periplasmic binding protein	8010	4705
b0656	689013	687997	<i>insH1</i>	IS5 transposase and trans-activator	3143	2558
b0657	690881	689343	<i>Int</i>	apolipoprotein N-acyltransferase	1343	1092
b0658	691784	690906	<i>ybeX</i>	putative ion transport	3502	3235
b0659	692341	691874	<i>ybeY</i>	ssRNA-specific endoribonuclease; 16S rRNA 3' end maturation and quality control co-endoribonuclease working with RNase R; rRNA transcription antitermination factor	963	684
b0660	693378	692338	<i>ybeZ</i>	heat shock protein, putative NTPase; PhoH-like protein	4559	3439
b0661	694955	693531	<i>miaB</i>	tRNA-i(6)A37 methylthiotransferase	2372	1005
b0662	695101	696276	<i>ubiF</i>	2-octaprenyl-3-methyl-6-methoxy-1,4-benzoquinol oxygenase	1460	658
b0674	699177	697513	<i>asnB</i>	asparagine synthetase B	4329	6598
b0675	700326	699574	<i>umpH</i>	UMP phosphatase	1390	576
b0676	701594	700374	<i>nagC</i>	N-acetylglucosamine-inducible nag divergent operon transcriptional repressor	2161	1181
b0677	702751	701603	<i>nagA</i>	N-acetylglucosamine-6-phosphate deacetylase	5573	895
b0678	703611	702811	<i>nagB</i>	glucosamine-6-phosphate deaminase	14647	543
b0679	703944	705890	<i>nagE</i>	N-acetyl glucosamine specific PTS enzyme IIC, IIB, and IIA components	22983	1025
b0680	706093	707757	<i>glnS</i>	glutamyl-tRNA synthetase	5572	2335
b0681	708334	709740	<i>chiP</i>	chitoporphin, uptake of chitosugars	529	250
b0682	709790	710116	<i>chiQ</i>	chitosugar-induced verified lipoprotein	81	190
b0683	710646	710200	<i>fur</i>	ferric iron uptake regulon transcriptional repressor; autorepressor	8151	8754
b0684	711465	710935	<i>fldA</i>	flavodoxin 1	2793	2236
b0685	711898	711605	<i>ybfE</i>	LexA-regulated protein, CopB family	112	159
b0686	712802	712038	<i>ybfF</i>	acyl-CoA esterase	354	476
b0687	712987	713532	<i>seqA</i>	negative modulator of initiation of replication	3029	1859
b0688	713558	715198	<i>pgm</i>	phosphoglucomutase	12380	3078
b0689	715412	715906	<i>ybfP</i>	lipoprotein	47	104
b0692	718265	716946	<i>potE</i>	putrescine/proton symporter: putrescine/ornithine antiporter	117	587
b0693	720460	718262	<i>speF</i>	ornithine decarboxylase isozyme, inducible	43	274
b0694	721733	721056	<i>kdpE</i>	response regulator in two-component regulatory system with KdpD	57	148
b0695	724414	721730	<i>kdpD</i>	fused sensory histidine kinase in two-component regulatory system with KdpE: signal sensing protein	281	1802
b0696	724979	724407	<i>kdpC</i>	potassium translocating ATPase, subunit C	46	876
b0697	727036	724988	<i>kdpB</i>	potassium translocating ATPase, subunit B	136	3042
b0698	728732	727059	<i>kdpA</i>	potassium translocating ATPase, subunit A	114	4402
b0699	729134	729340	<i>ybfA</i>	DUF2517 family protein	843	1762
b0700	729583	733776	<i>rhsC</i>	Rhs protein with putative toxin domain; putative neighboring cell growth inhibitor	317	1598
b0702	733776	734102	<i>ybfB</i>	putative membrane protein	31	1063
b0704	735650	736219	<i>ybfC</i>	putative secreted protein	88	1805
b0706	738092	738853	<i>ybfD</i>	H repeat-associated putative transposase	50	1178
b0707	739001	739510	<i>ybgA</i>	DUF1722 family protein	630	885
b0708	739507	740925	<i>phr</i>	deoxyribodipyrimidine photolyase, FAD-binding	736	1030
b0709	742556	741075	<i>dtpD</i>	dipeptide and tripeptide permease D	70	375
b0710	742827	743570	<i>ybgI</i>	NIF3 family metal-binding protein	784	612
b0711	743593	744249	<i>ybgJ</i>	putative allophanate hydrolase, subunit 1	661	402

b0712	744243	745175	<i>ybgK</i>	putative allophanate hydrolase, subunit 2	847	634
b0713	745165	745899	<i>ybgL</i>	UPF0271 family protein	289	237
b0714	745935	746726	<i>nei</i>	endonuclease VIII and 5-formyluracil/5-hydroxymethyluracil DNA glycosylase	243	156
b0715	747769	746723	<i>abrB</i>	regulator of aidB expression; inner membrane protein	477	268
b0716	748982	747921	<i>ybgO</i>	putative fimbrial protein	82	619
b0717	749707	748979	<i>ybgP</i>	putative periplasmic pilin chaperone	30	219
b0718	752169	749722	<i>ybgQ</i>	putative outer membrane protein	32	329
b0719	752795	752229	<i>ybgD</i>	putative fimbrial-like adhesin protein	44	178
b0720	754468	753185	<i>gltA</i>	citrate synthase	58439	18792
b0721	755177	755566	<i>sdhC</i>	succinate dehydrogenase, membrane subunit, binds cytochrome b556	7707	1120
b0722	755560	755907	<i>sdhD</i>	succinate dehydrogenase, membrane subunit, binds cytochrome b556	3036	639
b0723	755907	757673	<i>sdhA</i>	succinate dehydrogenase, flavoprotein subunit	24439	4294
b0724	757689	758405	<i>sdhB</i>	succinate dehydrogenase, FeS subunit	16895	4067
b0726	758706	761507	<i>sucA</i>	2-oxoglutarate decarboxylase, thiamine triphosphate-binding	55069	11310
b0727	761522	762739	<i>sucB</i>	dihydrolipoyltranssuccinase	37004	3980
b0728	763014	764180	<i>sucC</i>	succinyl-CoA synthetase, beta subunit	43226	6883
b0729	764180	765049	<i>sucD</i>	succinyl-CoA synthetase, NAD(P)-binding, alpha subunit	42983	7493
b0730	765875	765153	<i>mngR</i>	transcriptional repressor for the mannosyl-D-glycerate catabolic operon	283	437
b0731	765984	767960	<i>mngA</i>	fused 2-O-a-mannosyl-D-glycerate specific PTS enzymes: IIA component/IIB component/IIC component	27	162
b0732	767978	770611	<i>mngB</i>	alpha-mannosidase	385	1043
b0733	771458	773026	<i>cydA</i>	cytochrome d terminal oxidase, subunit I	42219	11280
b0734	773042	774181	<i>cydB</i>	cytochrome d terminal oxidase, subunit II	20560	4943
b0735	774309	774602	<i>ybgE</i>	putative inner membrane protein in cydABX-ybgE operon	2649	899
b0736	774752	775156	<i>ybgC</i>	acyl-CoA thioester hydrolase	979	1992
b0737	775153	775845	<i>tolQ</i>	membrane spanning protein in TolA-TolQ-TolR complex	2248	2277
b0738	775849	776277	<i>tolR</i>	membrane spanning protein in TolA-TolQ-TolR complex	714	623
b0739	776342	777607	<i>tolA</i>	membrane anchored protein in TolA-TolQ-TolR complex	2361	3676
b0740	777740	779032	<i>tolB</i>	periplasmic protein	18705	5098
b0741	779067	779588	<i>pal</i>	peptidoglycan-associated outer membrane lipoprotein	49138	10758
b0742	779598	780389	<i>ybgF</i>	periplasmic TolA-binding protein	7819	6227
b0750	782085	783128	<i>nadA</i>	quinolinate synthase, subunit A	475	3192
b0751	783166	783885	<i>pnuC</i>	nicotinamide riboside transporter	389	1037
b0752	784823	783882	<i>zitB</i>	zinc efflux system	451	913
b0753	785317	784937	<i>ybgS</i>	putative periplasmic protein	390	2289
b0754	785633	786685	<i>aroG</i>	3-deoxy-D-arabino-heptulosonate-7-phosphate synthase, phenylalanine repressible	3171	2335
b0755	787595	786843	<i>gpmA</i>	phosphoglyceromutase 1	25098	5151
b0756	788837	787797	<i>galM</i>	aldose 1-epimerase; type-1 mutarotase; galactose mutarotase	4330	947
b0757	789979	788831	<i>galK</i>	galactokinase	5819	1781
b0758	791029	789983	<i>galT</i>	galactose-1-phosphate uridylyltransferase	6699	271
b0759	792055	791039	<i>galE</i>	UDP-galactose-4-epimerase	12769	1158
b0760	793788	792316	<i>modF</i>	molybdate ABC transporter ATPase	674	1050
b0761	794644	793856	<i>modE</i>	transcriptional repressor for the molybdenum transport operon modABC	660	596
b0762	794773	794922	<i>acrZ</i>	AcrAB-TolC efflux pump accessory protein, membrane-associated	515	1654
b0763	795089	795862	<i>modA</i>	molybdate ABC transporter periplasmic binding protein; chlorate resistance protein	1165	838
b0764	795862	796551	<i>modB</i>	molybdate ABC transporter permease; chlorate resistance protein	356	270
b0765	796554	797612	<i>modC</i>	molybdate ABC transporter ATPase; chlorate resistance	478	458

				protein		
b0766	798431	797613	<i>ybhA</i>	pyridoxal phosphate (PLP) phosphatase	731	536
b0767	798586	799581	<i>pgl</i>	6-phosphogluconolactonase	2634	655
b0768	800575	799622	<i>ybhD</i>	putative DNA-binding transcriptional regulator	24	192
b0769	800759	801811	<i>ybhH</i>	putative PrpF family isomerase	7	32
b0770	801887	803320	<i>ybhI</i>	putative DASS family tricarboxylate or dicarboxylate transporter	8	193
b0771	803503	805764	<i>ybhJ</i>	aconitase family protein	95	474
b0772	807281	805998	<i>ybhC</i>	acyl-CoA thioesterase, lipoprotein	1846	1012
b0773	807909	807433	<i>ybhB</i>	kinase inhibitor homolog, UPF0098 family	1032	554
b0774	809257	807968	<i>bioA</i>	7,8-diaminopelargonic acid synthase, PLP-dependent	113	402
b0775	809344	810384	<i>bioB</i>	biotin synthase	275	1961
b0776	810381	811535	<i>bioF</i>	8-amino-7-oxononanoate synthase	77	381
b0777	811522	812277	<i>bioC</i>	malonyl-ACP O-methyltransferase, SAM-dependent	45	174
b0778	812270	812947	<i>bioD</i>	dethiobiotin synthetase	74	348
b0779	813526	815547	<i>uvrB</i>	exision nuclease of nucleotide excision repair, DNA damage recognition component	3029	2412
b0780	816647	815739	<i>ybhK</i>	putative CoD superfamily transferase	460	559
b0781	817044	818033	<i>moaA</i>	molybdopterin biosynthesis protein A	1125	1408
b0782	818055	818567	<i>moaB</i>	inactive molybdopterin adenyltransferase	1302	568
b0783	818570	819055	<i>moaC</i>	molybdopterin biosynthesis, protein C	866	359
b0784	819048	819293	<i>moaD</i>	molybdopterin synthase, small subunit	184	69
b0785	819295	819747	<i>moaE</i>	molybdopterin synthase, large subunit	678	395
b0786	819884	820588	<i>ybhL</i>	putative acetate transporter; BAX Inhibitor-1 family inner membrane protein	3249	2395
b0787	820793	821506	<i>ybhM</i>	BAX Inhibitor-1 family inner membrane protein	63	290
b0788	822498	821542	<i>ybhN</i>	UPF0104 family inner membrane protein	70	270
b0789	823739	822498	<i>clsB</i>	cardiolipin synthase 2	236	317
b0790	824497	823736	<i>ybhP</i>	endo/exonuclease/phosphatase family protein	181	336
b0791	824630	825040	<i>ybhQ</i>	inner membrane protein	1646	3308
b0792	826108	825002	<i>ybhR</i>	putative ABC transporter permease	487	1344
b0793	827252	826119	<i>ybhS</i>	putative ABC transporter permease	461	615
b0794	828981	827245	<i>ybhF</i>	putative ABC transporter ATPase	1446	603
b0795	829972	828974	<i>ybhG</i>	putative membrane fusion protein (MFP) component of efflux pump, membrane anchor	2936	523
b0796	830643	829972	<i>ybiH</i>	DUF1956 domain-containing tetR family putative transcriptional regulator	1490	525
b0797	830872	832236	<i>rhIE</i>	ATP-dependent RNA helicase	478	444
b0798	832950	832468	<i>ybiA</i>	DUF1768 family protein	579	296
b0799	833070	835220	<i>dinG</i>	ATP-dependent DNA helicase	593	686
b0800	835248	836210	<i>ybiB</i>	putative family 3 glycosyltransferase	1193	595
b0801	836351	837436	<i>ybiC</i>	putative dehydrogenase	1446	1275
b0802	837925	837665	<i>ybiJ</i>	DUF1471 family putative periplasmic protein	210	191
b0803	838456	838190	<i>ybiI</i>	DksA-type zinc finger protein	209	286
b0804	839207	838530	<i>ybiX</i>	Fe(II)-dependent oxygenase superfamily protein	426	131
b0805	841531	839249	<i>fiu</i>	catecholate siderophore receptor	3737	305
b0806	842056	841796	<i>mcbA</i>	colanic acid mucoidy stimulation protein	76	653
b0807	842332	843258	<i>rlmF</i>	23S rRNA m(6)A1618 methyltransferase, SAM-dependent	175	349
b0808	845480	843255	<i>ybiO</i>	mechanosensitive channel protein, intermediate conductance	296	779
b0809	846463	845741	<i>glnQ</i>	glutamine transporter subunit	1653	625
b0810	847119	846460	<i>glnP</i>	glutamine transporter subunit	1141	762
b0811	848004	847258	<i>glnH</i>	glutamine transporter subunit	10909	10431
b0812	848911	848408	<i>dps</i>	Fe-binding and storage protein; stress-inducible DNA-binding protein	18158	24153

b0813	850097	849210	<i>rhtA</i>	threonine and homoserine efflux system	254	537
b0814	850450	850965	<i>ompX</i>	outer membrane protein X	28670	15616
b0815	852597	851014	<i>opgE</i>	OPG biosynthetic transmembrane phosphoethanolamine transferase	538	842
b0817	853183	853650	<i>mntR</i>	Mn(2+)-responsive manganese regulon transcriptional regulator	702	1071
b0818	853647	854765	<i>ybiR</i>	putative transporter	367	424
b0819	855744	854824	<i>ldtB</i>	L,D-transpeptidase linking Lpp to murein	2182	2614
b0820	855963	857555	<i>ybiT</i>	ABC-F family putative regulatory ATPase	1313	1331
b0821	859061	857796	<i>ybiU</i>	DUF1479 family protein	786	104
b0822	860028	859213	<i>ybiV</i>	sugar phosphatase; fructose-1-P/ribose-5-P/glucose-6-P phosphatase	431	451
b0823	862606	860174	<i>ybiW</i>	putative pyruvate formate lyase	409	174
b0824	863511	862612	<i>ybiY</i>	putative pyruvate formate lyase activating enzyme	74	94
b0825	863642	864304	<i>fsaA</i>	fructose-6-phosphate aldolase 1	235	87
b0826	865129	864380	<i>moeB</i>	molybdopterin synthase sulfurylase	460	215
b0827	866364	865129	<i>moeA</i>	molybdopterin molybdenumtransferase; molybdopterin biosynthesis protein	994	362
b0828	866568	867533	<i>iaaA</i>	Isoaspartyl peptidase	2487	4986
b0829	867520	869391	<i>gsiA</i>	glutathione ABC transporter ATPase	2268	2695
b0830	869411	870949	<i>gsiB</i>	glutathione ABC transporter periplasmic binding protein	3129	2731
b0831	870967	871887	<i>gsiC</i>	glutathione ABC transporter permease	653	610
b0832	871890	872801	<i>gsiD</i>	glutathione ABC transporter permease	287	293
b0833	872979	875327	<i>yliE</i>	putative membrane-anchored cyclic-di-GMP phosphodiesterase	162	734
b0834	875335	876663	<i>yliF</i>	putative membrane-anchored diguanylate cyclase	79	528
b0835	878035	876710	<i>rimO</i>	ribosomal protein S12 methylthiotransferase	715	742
b0836	878248	878631	<i>bssR</i>	repressor of biofilm formation by indole transport regulation	9177	38537
b0837	878742	879857	<i>yliI</i>	soluble aldose sugar dehydrogenase	250	1516
b0838	880480	879854	<i>gstB</i>	glutathione S-transferase	1757	1117
b0839	880727	881929	<i>dacC</i>	D-alanyl-D-alanine carboxypeptidase; penicillin-binding protein 6a	2695	2683
b0840	882734	881976	<i>deoR</i>	deoxyribose-5-phosphate-inducible deoxyribose operon transcriptional repressor; repressor of nupG and tsx	980	1124
b0841	883388	882792	<i>ybjG</i>	undecaprenyl pyrophosphate phosphatase	2478	1782
b0842	883673	884905	<i>mdfA</i>	multidrug efflux system protein	585	616
b0843	885230	884946	<i>ybjH</i>	uncharacterized protein	102	188
b0844	886131	885316	<i>ybjI</i>	5-amino-6-(5-phospho-D-ribitylamino)uracil phosphatase; pyrimidine phosphatase; riboflavin synthesis	615	575
b0845	887339	886131	<i>ybjJ</i>	putative drug efflux MFS transporter, inner membrane protein	141	223
b0846	887423	887959	<i>rcdA</i>	transcriptional regulator of csgD and ybiJI; autoregulator	189	198
b0847	889819	888134	<i>ybjL</i>	putative transporter	766	1906
b0848	890089	890466	<i>ybjM</i>	inner membrane protein	104	156
b0849	890753	890496	<i>grxA</i>	glutaredoxin 1, redox coenzyme for ribonucleotide reductase (RNR1a)	271	660
b0850	890913	891200	<i>ybjC</i>	DUF1418 family protein	296	505
b0851	891184	891906	<i>nfsA</i>	nitroreductase A, NADPH-dependent, FMN-dependent	928	676
b0852	891967	892869	<i>rimK</i>	ribosomal protein S6 modification protein	623	654
b0853	892957	893433	<i>ybjN</i>	negative regulator of motility; multicopy suppressor of coaA(Ts)	1715	1342
b0854	893784	894896	<i>potF</i>	putrescine ABC transporter periplasmic binding protein	937	1050
b0855	894991	896124	<i>potG</i>	putrescine ABC transporter ATPase	214	171
b0856	896134	897087	<i>potH</i>	putrescine ABC transporter permease	154	139
b0857	897084	897929	<i>potI</i>	putrescine ABC transporter permease	125	131
b0858	897989	898477	<i>ybjO</i>	DUF2593 family inner membrane protein	108	238

b0859	898518	899645	<i>rlmC</i>	23S rRNA m(5)U747 methyltransferase, SAM-dependent	125	230
b0860	900575	899844	<i>artJ</i>	arginine ABC transporter periplasmic binding protein	291	11607
b0861	901534	900866	<i>artM</i>	arginine ABC transporter permease	319	551
b0862	902250	901534	<i>artQ</i>	arginine ABC transporter permease	363	458
b0863	902988	902257	<i>artI</i>	arginine transporter subunit	3274	3688
b0864	903734	903006	<i>artP</i>	arginine ABC transporter ATPase	1045	1754
b0865	904467	903952	<i>ybjP</i>	lipoprotein	2213	1671
b0866	904593	904916	<i>ybjQ</i>	UPF0145 family protein	993	848
b0867	904913	905743	<i>amiD</i>	1,6-anhydro-N-acetylmuramyl-L-alanine amidase, Zn-dependent; OM lipoprotein	582	408
b0868	906753	905740	<i>ybjS</i>	putative NAD(P)H-dependent oxidoreductase	797	872
b0869	908282	906852	<i>ybjT</i>	putative NAD-dependent oxidoreductase	597	525
b0870	909294	908293	<i>ltaE</i>	L-allo-threonine aldolase, PLP-dependent	1739	1033
b0871	911049	909331	<i>poxB</i>	pyruvate dehydrogenase, thiamine triphosphate-binding, FAD-binding	2265	2724
b0872	912150	911182	<i>hcr</i>	HCP oxidoreductase, NADH-dependent	402	67
b0873	913814	912162	<i>hcp</i>	hybrid-cluster [4Fe-2S-2O] subunit of anaerobic terminal reductases	1410	170
b0874	914857	913958	<i>ybjE</i>	putative transporter	313	461
b0875	916047	915352	<i>aqpZ</i>	aquaporin Z	453	408
b0876	916473	918131	<i>ybjD</i>	putative OLD family ATP-dependent endonuclease; DUF2813 family protein	4877	1159
b0877	919120	918128	<i>ybjX</i>	DUF535 family protein	640	2089
b0878	919235	920350	<i>macA</i>	macrolide transporter membrane fusion protein (MFP) component	563	759
b0879	920347	922293	<i>macB</i>	macrolide ABC transporter peremase/ATPase	481	893
b0880	922590	922366	<i>cspD</i>	inhibitor of DNA replication, cold shock protein homolog	9877	30566
b0881	922913	923233	<i>clpS</i>	regulatory protein for ClpA substrate specificity	1753	8994
b0882	923264	925540	<i>clpA</i>	ATPase and specificity subunit of ClpA-ClpP ATP-dependent serine protease, chaperone activity	35300	19920
b0884	926443	926225	<i>infA</i>	translation initiation factor IF-1	5582	4469
b0885	927432	926728	<i>aat</i>	leucyl/phenylalanyl-tRNA-protein transferase	306	268
b0886	929195	927474	<i>cydC</i>	glutathione/cysteine ABC transporter export permease/ATPase	1256	1295
b0887	930962	929196	<i>cydD</i>	glutathione/cysteine ABC transporter export permease/ATPase	747	995
b0888	932050	931085	<i>trxB</i>	thioredoxin reductase, FAD/NAD(P)-binding	5674	1419
b0889	932595	933089	<i>lrp</i>	leucine-responsive global transcriptional regulator	5076	4547
b0890	933224	937213	<i>ftsK</i>	DNA translocase at septal ring sorting daughter chromosomes	6776	4722
b0891	937372	937983	<i>lolA</i>	lipoprotein chaperone	2984	1098
b0892	937994	939337	<i>rarA</i>	recombination intermediate processing DNA-dependent ATPase	762	553
b0893	939428	940720	<i>serS</i>	seryl-tRNA synthetase	16852	5008
b0894	940959	943403	<i>dmsA</i>	dimethyl sulfoxide reductase, anaerobic, subunit A	7920	938
b0895	943414	944031	<i>dmsB</i>	dimethyl sulfoxide reductase, anaerobic, subunit B	1067	163
b0896	944033	944896	<i>dmsC</i>	dimethyl sulfoxide reductase, anaerobic, subunit C	1146	195
b0897	945557	944931	<i>ycaC</i>	putative isochorismatase family hydrolase	3198	1813
b0898	945871	947019	<i>ycaD</i>	putative MFS transporter, inner membrane protein	558	1860
b0899	947229	948659	<i>ycaM</i>	putative transporter	747	666
b0900	949568	948660	<i>ycaN</i>	LysR family putative transcriptional regulator	106	330
b0901	949668	950258	<i>ycaK</i>	putative NAD(P)H-dependent oxidoreductase	88	162
b0902	951080	950340	<i>pflA</i>	pyruvate formate-lyase 1-activating enzyme; [formate-C-acetyltransferase 1]-activating enzyme; PFL activase	5759	3046
b0903	953554	951272	<i>pflB</i>	formate C-acetyltransferase 1, anaerobic; pyruvate formate-lyase 1	238650	53154
b0904	954466	953609	<i>focA</i>	formate channel	11944	6513
b0905	956632	954872	<i>ycaO</i>	ribosomal protein S12 methylthiotransferase accessory factor	4846	884

b0906	956762	957454	<i>ycaP</i>	UPF0702 family putative inner membrane protein	733	814
b0907	957653	958741	<i>serC</i>	3-phosphoserine/phosphohydroxythreonine aminotransferase	4057	1849
b0908	958812	960095	<i>aroA</i>	5-enolpyruvylshikimate-3-phosphate synthetase	1101	759
b0909	960264	961028	<i>ycaL</i>	putative peptidase-related chaperone	68	157
b0910	961201	961884	<i>cmk</i>	cytidylate kinase	1237	901
b0911	961995	963668	<i>rpsA</i>	30S ribosomal subunit protein S1	164089	42344
b0912	963828	964112	<i>ihfB</i>	integration host factor (IHF), DNA-binding protein, beta subunit	1836	5284
b0913	964320	966584	<i>ycaI</i>	ComEC family inner membrane protein	382	1027
b0914	966621	968369	<i>msbA</i>	lipid ABC transporter permease/ATPase	1779	2210
b0915	968366	969352	<i>lpxK</i>	lipid A 4'kinase	294	207
b0916	969389	970621	<i>ycaQ</i>	DUF1006 family protein with C-terminal wHTH domain	208	347
b0917	970673	970855	<i>ycaR</i>	peroxide and acid resistance protein, UPF0434 family	230	130
b0918	970852	971598	<i>kdsB</i>	3-deoxy-manno-octulosonate cytidyltransferase	1338	542
b0919	971752	972645	<i>ycbJ</i>	protein kinase-like domain protein	6593	2577
b0920	973401	972622	<i>elyC</i>	envelope biogenesis factor; DUF218 superfamily protein	848	410
b0921	973537	974322	<i>smtA</i>	putative S-adenosyl-L-methionine-dependent methyltransferase	838	1027
b0922	974319	975641	<i>mukF</i>	chromosome condensin MukBEF, kleisin-like subunit, binds calcium	1189	1033
b0923	975622	976326	<i>mukE</i>	chromosome condensin MukBEF, Muke localization factor	1351	843
b0924	976326	980786	<i>mukB</i>	chromosome condensin MukBEF, ATPase and DNA-binding subunit	8020	3011
b0925	981047	982894	<i>ldtD</i>	murein L,D-transpeptidase	3292	2240
b0926	983075	983623	<i>ycbK</i>	M15A protease-related family periplasmic protein	1399	3123
b0927	983650	984297	<i>ycbL</i>	putative metal-binding enzyme	1138	1487
b0928	985709	984519	<i>aspC</i>	aspartate aminotransferase, PLP-dependent	12014	3794
b0929	986982	985894	<i>ompF</i>	outer membrane porin 1a (Ia;b;F)	555114	253939
b0930	988985	987585	<i>asnS</i>	asparaginyl tRNA synthetase	11919	6599
b0931	990356	989154	<i>pncB</i>	nicotinate phosphoribosyltransferase	2137	6265
b0932	990622	993234	<i>pepN</i>	aminopeptidase N	14998	3958
b0933	994044	993277	<i>ssuB</i>	aliphatic sulfonate ABC transporter ATPase	109	157
b0934	994832	994041	<i>ssuC</i>	aliphatic sulfonate ABC transporter permease	7	48
b0935	995988	994843	<i>ssuD</i>	alkanesulfonate monooxygenase, FMNH(2)-dependent	43	38
b0936	996944	995985	<i>ssuA</i>	aliphatic sulfonate ABC transporter periplasmic binding protein	32	37
b0937	997512	996937	<i>ssuE</i>	NAD(P)H-dependent FMN reductase	54	126
b0938	997868	998407	<i>elfA</i>	laminin-binding fimbrin subunit	92	272
b0939	998490	999191	<i>elfD</i>	putative periplasmic pilin chaperone	8	74
b0940	999216	1001816	<i>elfC</i>	putative outer membrane fimbrial subunit export usher protein	97	598
b0941	1001807	1002877	<i>elfG</i>	putative fimbrial-like adhesin protein	139	474
b0942	1002889	1003431	<i>ycbU</i>	putative fimbriae protein	34	101
b0943	1003439	1003954	<i>ycbV</i>	putative fimbrial-like adhesin protein	23	80
b0944	1003947	1004657	<i>ycbF</i>	putative periplasmic pilin chaperone	121	244
b0945	1004768	1005778	<i>pyrD</i>	dihydro-orotate oxidase, FMN-linked	444	311
b0946	1005952	1006494	<i>zapC</i>	FtsZ stabilizer	781	551
b0947	1007600	1006491	<i>ycbX</i>	6-N-hydroxylaminopurine detoxification oxidoreductase	1236	1361
b0948	1007844	1009952	<i>rlmL</i>	23S rRNA m(2)G2445 and m(7)G2069 methyltransferases, SAM-dependent	1466	1047
b0949	1009964	1011871	<i>uup</i>	replication regulatory ABC-F family DNA-binding ATPase	2525	1556
b0950	1012001	1013254	<i>pqiA</i>	paraquat-inducible, SoxRS-regulated inner membrane protein	694	893
b0951	1013259	1014899	<i>pqiB</i>	paraquat-inducible, SoxRS-regulated MCE domain protein	1723	1492

b0952	1014896	1015459	<i>pqiC</i>	DUF330 family putative lipoprotein	1382	771
b0953	1015715	1015882	<i>rmf</i>	ribosome modulation factor	4118	149375
b0954	1016470	1015952	<i>fabA</i>	beta-hydroxydecanoyl thioester dehydrase	3366	1670
b0955	1018299	1016539	<i>ycbZ</i>	putative peptidase	2069	1431
b0956	1018485	1018937	<i>matP</i>	Ter macrodomain organizer matS-binding protein	1860	1378
b0957	1020053	1019013	<i>ompA</i>	outer membrane protein A (3a;II*;G;d)	232632	66304
b0958	1020919	1020410	<i>sulA</i>	SOS cell division inhibitor	1246	4057
b0959	1021138	1021767	<i>sxy</i>	CRP-S-dependent promoter expression factor	385	1177
b0960	1023883	1021730	<i>yccS</i>	putative transporter, FUSC superfamily inner membrane protein	555	1040
b0961	1024348	1023902	<i>yccF</i>	DUF307 family inner membrane protein	114	214
b0962	1024471	1026525	<i>helD</i>	DNA helicase IV	1282	1216
b0963	1027015	1026557	<i>mgsA</i>	methylglyoxal synthase	11707	1901
b0964	1027773	1027111	<i>yccT</i>	UPF0319 family protein	141	297
b0965	1027946	1028359	<i>yccU</i>	putative CoA-binding protein	1858	1140
b0966	1028721	1028404	<i>hspQ</i>	heat shock protein involved in degradation of mutant DnaA; hemimethylated oriC DNA-binding protein	3956	4236
b0967	1029969	1028779	<i>rlmI</i>	23S rRNA m(5)C1962 methyltransferase, SAM-dependent	1351	801
b0968	1030064	1030342	<i>yccX</i>	weak acylphosphatase	316	677
b0969	1030668	1030339	<i>tusE</i>	mn(5)-s(2)U34-tRNA 2-thiolation sulfurtransferase	474	627
b0970	1031418	1030759	<i>yccA</i>	Modulator of FtsH protease, inner membrane protein	2378	6258
b0972	1032139	1033257	<i>hyaA</i>	hydrogenase 1, small subunit	115	48
b0973	1033254	1035047	<i>hyaB</i>	hydrogenase 1, large subunit	92	65
b0974	1035066	1035773	<i>hyaC</i>	hydrogenase 1, b-type cytochrome subunit	46	95
b0975	1035770	1036357	<i>hyaD</i>	hydrogenase 1 maturation protease	45	50
b0976	1036354	1036752	<i>hyaE</i>	putative HyaA chaperone	23	25
b0977	1036749	1037606	<i>hyaF</i>	hydrogenase-1 protein nickel incorporation factor	69	70
b0978	1037740	1039284	<i>cbdA</i>	cytochrome bd-II oxidase, subunit I	164	130
b0979	1039296	1040432	<i>cbdB</i>	cytochrome bd-II oxidase, subunit II	115	175
b0980	1040617	1041915	<i>appA</i>	phosphoanhydride phosphorylase	228	243
b0981	1044210	1042030	<i>etk</i>	tyrosine-protein kinase, role in O-antigen capsule formation	242	508
b0982	1044676	1044230	<i>etp</i>	O-antigen capsule forming protein-tyrosine-phosphatase; Etk-P dephosphorylase	33	56
b0983	1045803	1044664	<i>gfcE</i>	putative O-antigen capsule outer membrane auxillary protein export channel	84	135
b0984	1047945	1045849	<i>gfcD</i>	putative O-antigen capsule production periplasmic protein	65	204
b0985	1048691	1047945	<i>gfcC</i>	putative O-antigen capsule production periplasmic protein	7	32
b0986	1049332	1048688	<i>gfcB</i>	O-antigen capsule production lipoprotein	5	40
b0987	1049744	1049439	<i>gfcA</i>	O-antigen capsule production threonine-rich inner membrane protein	35	50
b0988	1050027	1050530	<i>insB1</i>	IS1 transposase B	69	199
b0989	1051175	1050963	<i>cspH</i>	stress protein, member of the CspA-family	12	63
b0990	1051461	1051673	<i>cspG</i>	cold shock protein homolog, cold-inducible	80	246
b0991	1051847	1052077	<i>ymcE</i>	cold shock gene	4	43
b0992	1053362	1052289	<i>yccM</i>	putative 4Fe-4S membrane protein	742	295
b0993	1056178	1053434	<i>torS</i>	hybrid sensory histidine kinase in two-component regulatory system with TorR	123	368
b0994	1056261	1057289	<i>torT</i>	periplasmic sensory protein associated with the TorRS two-component regulatory system	181	179
b0995	1057954	1057262	<i>torR</i>	response regulator in two-component regulatory system with TorS	214	269
b0996	1058084	1059256	<i>torC</i>	trimethylamine N-oxide (TMAO) reductase I, cytochrome c-type subunit	18	98
b0997	1059256	1061802	<i>torA</i>	trimethylamine N-oxide (TMAO) reductase I, catalytic subunit	67	248

b0998	1061799	1062398	<i>torD</i>	TorA-maturation chaperone	40	71
b0999	1062855	1062550	<i>cbpM</i>	modulator of CbpA co-chaperone	234	117
b1000	1063775	1062855	<i>cbpA</i>	DnaK co-chaperone; curved DNA-binding protein	1925	1084
b1001	1064036	1065292	<i>yccE</i>	uncharacterized protein	46	350
b1002	1065585	1066826	<i>agp</i>	glucose-1-phosphatase/inositol phosphatase	15735	3325
b1003	1067091	1066864	<i>yccJ</i>	uncharacterized protein	10514	4193
b1004	1067708	1067112	<i>wrbA</i>	NAD(P)H:quinone oxidoreductase	23351	7705
b1006	1069839	1068511	<i>rutG</i>	pyrimidine permease	61	275
b1007	1070354	1069860	<i>rutF</i>	flavin:NADH reductase	14	20
b1008	1070955	1070365	<i>rutE</i>	putative malonic semialdehyde reductase	6	24
b1009	1071765	1070965	<i>rutD</i>	putative reactive intermediate detoxifying aminoacrylate hydrolase	5	25
b1010	1072159	1071773	<i>rutC</i>	putative aminoacrylate deaminase, reactive intermediate detoxification; weak enamine/imine deaminase activity	5	30
b1011	1072863	1072171	<i>rutB</i>	ureidoacrylate amidohydrolase	7	23
b1012	1074011	1072863	<i>rutA</i>	pyrimidine oxygenase, FMN-dependent	9	47
b1013	1074242	1074880	<i>rutR</i>	rut operon transcriptional repressor for	363	414
b1014	1078882	1074920	<i>putA</i>	fused DNA-binding transcriptional regulator/proline dehydrogenase/pyrroline-5-carboxylate dehydrogenase	29271	6873
b1015	1079305	1080813	<i>putP</i>	proline:sodium symporter	7743	2172
b1018	1082243	1083370	<i>efeO</i>	inactive ferrous ion transporter EfeUOB	2689	252
b1019	1083376	1084647	<i>efeB</i>	deferrochelate, periplasmic	1190	169
b1020	1084992	1086056	<i>phoH</i>	ATP-binding protein; putative PhoH family P-loop ATPase	9726	10204
b1021	1086519	1086106	<i>pgaD</i>	biofilm PGA synthase PgaCD, regulatory subunit; c-di-GMP-stimulated activity and dimerization	108	232
b1022	1087846	1086521	<i>pgaC</i>	biofilm PGA synthase PgaCD, catalytic subunit; poly-beta-1,6-N-acetyl-D-glucosamine synthase	92	417
b1023	1089857	1087839	<i>pgaB</i>	poly-beta-1,6-N-acetyl-D-glucosamine (PGA) N-deacetylase outer membrane export lipoprotein	84	299
b1024	1092289	1089866	<i>pgaA</i>	biofilm adhesin polysaccharide PGA secretin; OM porin; poly-beta-1,6-N-acetyl-D-glucosamine export protein	170	687
b1025	1092876	1094234	<i>ycdT</i>	diguanylate cyclase, membrane-anchored	110	1507
b1026	1095141	1094275	<i>insF1</i>	IS3 transposase B	106	239
b1027	1095437	1095138	<i>insE1</i>	IS3 transposase A	106	309
b1029	1095843	1096829	<i>ycdU</i>	putative inner membrane protein	12	890
b1033	1097886	1098824	<i>ghrA</i>	glyoxylate/hydroxypyruvate reductase A	931	883
b1034	1098879	1099616	<i>ycdX</i>	alkaline phosphatase	1325	1196
b1035	1099640	1100194	<i>ycdY</i>	redox enzyme maturation protein (REMP) chaperone for YcdX	1087	446
b1036	1100296	1100787	<i>ycdZ</i>	DUF1097 family inner membrane protein	721	337
b1037	1101684	1100851	<i>csgG</i>	curli production assembly/transport outer membrane lipoprotein	204	1120
b1038	1102127	1101711	<i>csgF</i>	curli nucleation outer membrane protein	124	1032
b1039	1102541	1102152	<i>csgE</i>	curlin secretion specificity factor	100	1235
b1040	1103196	1102546	<i>csgD</i>	csgBAC operon transcriptional regulator	222	3388
b1041	1103951	1104406	<i>csgB</i>	curlin nucleator protein, minor subunit in curli complex	51	6811
b1042	1104447	1104902	<i>csgA</i>	curlin subunit, amyloid curli fibers, cryptic	224	11073
b1043	1104961	1105293	<i>csgC</i>	curli assembly protein	6	117
b1044	1105414	1105725	<i>ymdA</i>	uncharacterized protein	114	334
b1045	1105820	1106353	<i>ymdB</i>	O-acetyl-ADP-ribose deacetylase; RNase III inhibitor during cold shock; putative cardiolipin synthase C regulatory subunit	611	1090
b1046	1106355	1107776	<i>clsC</i>	stationary phase cardiolipin synthase 3	446	955
b1047	1108941	1107784	<i>opgC</i>	OPG biosynthetic transmembrane succinyltransferase	437	1085
b1048	1109335	1110870	<i>opgG</i>	OPG biosynthetic periplasmic beta-1,6 branching glycosyltransferase	8230	11311
b1049	1110863	1113406	<i>opgH</i>	OPG biosynthetic ACP-dependent transmembrane UDP-glucose beta-1,2 glycosyltransferase; nutrient-dependent	4527	2092

				cell size regulator, FtsZ assembly antagonist		
b1050	1113579	1113806	<i>yceK</i>	outer membrane integrity lipoprotein	561	621
b1051	1114181	1113807	<i>msyB</i>	multicopy suppressor of secY and secA	2617	2264
b1053	1115490	1114264	<i>mdtG</i>	putative drug efflux system protein	265	443
b1054	1116582	1115662	<i>lpxL</i>	lauryl-acyl carrier protein (ACP)-dependent acyltransferase	816	1094
b1055	1116807	1117859	<i>yceA</i>	putative rhodanese-related sulfurtransferase	1211	1251
b1056	1118476	1117901	<i>yceI</i>	periplasmic high pH-inducible lipid-binding protein	70	218
b1057	1119046	1118480	<i>yceJ</i>	putative cytochrome b561	18	64
b1058	1119447	1119307	<i>yceO</i>	uncharacterized protein	4	723
b1059	1120586	1119468	<i>solA</i>	N-methyltryptophan oxidase, FAD-binding	1386	979
b1060	1120955	1120701	<i>bssS</i>	biofilm regulator	9747	15586
b1061	1121487	1121242	<i>dinI</i>	DNA damage-inducible protein I	410	336
b1062	1122607	1121561	<i>pyrC</i>	dihydro-orotase	2605	1160
b1063	1123273	1122713	<i>yceB</i>	lipoprotein, DUF1439 family	3710	2835
b1064	1124054	1123407	<i>grxB</i>	glutaredoxin 2 (Grx2)	3036	3605
b1065	1125326	1124118	<i>mdtH</i>	multidrug resistance efflux transporter conferring overexpression resistance to norfloxacin and enoxacin	220	177
b1066	1125562	1126146	<i>rimJ</i>	ribosomal-protein-S5-alanine N-acetyltransferase	2565	1088
b1067	1126157	1126804	<i>yceH</i>	UPF0502 family protein	3139	564
b1068	1126806	1127729	<i>yceM</i>	putative oxidoreductase	1126	314
b1069	1127839	1129374	<i>murJ</i>	putative lipid II flippase	589	1611
b1070	1129830	1129414	<i>flgN</i>	export chaperone for FlgK and FlgL	1669	7065
b1071	1130128	1129835	<i>flgM</i>	anti-sigma factor for FliA (sigma 28)	1084	3116
b1072	1130863	1130204	<i>flgA</i>	assembly protein for flagellar basal-body periplasmic P ring	721	3327
b1073	1131018	1131434	<i>flgB</i>	flagellar component of cell-proximal portion of basal-body rod	1186	3551
b1074	1131438	1131842	<i>flgC</i>	flagellar component of cell-proximal portion of basal-body rod	985	1689
b1075	1131854	1132549	<i>flgD</i>	flagellar hook assembly protein	2912	4865
b1076	1132574	1133782	<i>flgE</i>	flagellar hook protein	6532	9171
b1077	1133802	1134557	<i>flgF</i>	flagellar component of cell-proximal portion of basal-body rod	1025	850
b1078	1134729	1135511	<i>flgG</i>	flagellar component of cell-distal portion of basal-body rod	3612	3304
b1079	1135564	1136262	<i>flgH</i>	flagellar protein of basal-body outer-membrane L ring	554	622
b1080	1136274	1137371	<i>flgI</i>	putative flagellar basal body protein	837	1742
b1081	1137371	1138312	<i>flgJ</i>	flagellar rod assembly protein and murein hydrolase; flagellum-specific muramidase	412	914
b1082	1138378	1140021	<i>flgK</i>	flagellar hook-filament junction protein 1	3652	4131
b1083	1140033	1140986	<i>flgL</i>	flagellar hook-filament junction protein	6834	5814
b1084	1144367	1141182	<i>rne</i>	endoribonuclease; RNA-binding protein;RNA degradosome binding protein	13225	4972
b1085	1144502	1144822	<i>yceQ</i>	uncharacterized protein	645	629
b1086	1144940	1145899	<i>rluC</i>	23S rRNA pseudouridine(955,2504,2580) synthase	708	1211
b1087	1146595	1146011	<i>yceF</i>	m(7)GTP pyrophosphatase	1416	2846
b1088	1146794	1147315	<i>yceD</i>	DUF177 family protein	5577	4651
b1089	1147367	1147540	<i>rpmF</i>	50S ribosomal subunit protein L32	12208	3390
b1090	1147621	1148691	<i>plsX</i>	putative phosphate acyltransferase	1180	2151
b1091	1148759	1149712	<i>fabH</i>	3-oxoacyl-[acyl-carrier-protein] synthase III	4405	1169
b1092	1149728	1150657	<i>fabD</i>	malonyl-CoA-[acyl-carrier-protein] transacylase	9609	1938
b1093	1150670	1151404	<i>fabG</i>	3-oxoacyl-[acyl-carrier-protein] reductase	14702	6418
b1094	1151615	1151851	<i>acpP</i>	acyl carrier protein (ACP)	36692	17403
b1095	1151939	1153180	<i>fabF</i>	3-oxoacyl-[acyl-carrier-protein] synthase II	15406	6824
b1096	1153300	1154109	<i>pabC</i>	4-amino-4-deoxychorismate lyase component of para-aminobenzoate synthase multienzyme complex	472	753

b1097	1154112	1155134	<i>yceG</i>	septation protein, ampicillin sensitivity	286	669
b1098	1155124	1155765	<i>tmk</i>	thymidylate kinase	292	323
b1099	1155762	1156766	<i>holB</i>	DNA polymerase III, delta prime subunit	317	401
b1100	1156777	1157574	<i>ycfH</i>	putative DNase	1480	3387
b1101	1157869	1159302	<i>ptsG</i>	fused glucose-specific PTS enzymes: IIB component/IIC component	55956	7579
b1102	1161551	1159362	<i>fhuE</i>	ferric-rhodotorulic acid outer membrane transporter	534	1323
b1103	1161885	1162244	<i>hinT</i>	purine nucleoside phosphoramidase, dadA activator protein	1059	389
b1104	1162247	1162624	<i>ycfL</i>	uncharacterized protein	926	456
b1105	1162638	1163279	<i>lpoB</i>	OM lipoprotein stimulator of MrcB transpeptidase	2650	916
b1106	1163260	1164084	<i>thiK</i>	thiamine kinase	296	343
b1107	1164095	1165120	<i>nagZ</i>	beta N-acetyl-glucosaminidase	2435	1096
b1108	1165143	1165685	<i>ycfP</i>	putative UPF0227 family esterase	9845	4257
b1109	1166085	1167389	<i>ndh</i>	respiratory NADH dehydrogenase 2/cupric reductase	1948	1181
b1110	1167599	1168138	<i>ycfJ</i>	uncharacterized protein	2197	1457
b1111	1168832	1168200	<i>ycfQ</i>	repressor for bhsA(ycfR)	851	3140
b1112	1169073	1169330	<i>bhsA</i>	biofilm, cell surface and signaling protein	350	1278
b1113	1170374	1169412	<i>ldtC</i>	L,D-transpeptidase linking Lpp to murein	220	2205
b1114	1173964	1170518	<i>mfd</i>	transcription-repair coupling factor	3690	2329
b1115	1175165	1174092	<i>ycfT</i>	inner membrane protein	44	252
b1116	1175427	1176626	<i>lolC</i>	lipoprotein-releasing system transmembrane protein	687	560
b1117	1176619	1177320	<i>lolD</i>	outer membrane-specific lipoprotein transporter subunit	552	224
b1118	1177320	1178564	<i>lolE</i>	lipoprotein-releasing system transmembrane protein	1140	1292
b1119	1178593	1179504	<i>nagK</i>	N-acetyl-D-glucosamine kinase	938	562
b1120	1179631	1180359	<i>cobB</i>	deacetylase of acs and cheY, chemotaxis regulator	1808	569
b1121	1181267	1180479	<i>ycfZ</i>	inner membrane protein	19	93
b1122	1181725	1181264	<i>ymfA</i>	DUF3592 family inner membrane protein	36	84
b1123	1182829	1181783	<i>potD</i>	spermidine/putrescine ABC transporter periplasmic binding protein	9351	3835
b1124	1183620	1182826	<i>potC</i>	spermidine/putrescine ABC transporter permease	965	716
b1125	1184444	1183617	<i>potB</i>	spermidine/putrescine ABC transporter permease	362	235
b1126	1185594	1184458	<i>potA</i>	spermidine/putrescine ABC transporter ATPase	711	703
b1127	1185844	1187070	<i>pepT</i>	peptidase T	6434	2188
b1128	1188240	1187119	<i>roxA</i>	50S ribosomal protein L16 arginine hydroxylase; 2-oxoglutarate oxygenase	4404	1859
b1129	1189776	1188316	<i>phoQ</i>	sensory histidine kinase in two-component regulatory system with PhoP	903	1378
b1130	1190447	1189776	<i>phoP</i>	response regulator in two-component regulatory system with PhoQ	2997	3239
b1131	1191986	1190616	<i>purB</i>	adenylosuccinate lyase	5632	1207
b1132	1192631	1191990	<i>hflD</i>	putative lysogenization regulator	881	502
b1133	1193773	1192667	<i>mnmA</i>	tRNA(Gln,Lys,Glu) U34 2-thiouridylase	1282	1042
b1134	1194288	1193827	<i>nudJ</i>	bifunctional thiamine pyrimidine pyrophosphate hydrolase and thiamine pyrophosphate hydrolase	225	167
b1135	1194951	1194298	<i>rluE</i>	23S rRNA pseudouridine(2457) synthase	147	488
b1136	1195123	1196373	<i>icd</i>	isocitrate dehydrogenase; e14 prophage attachment site; tellurite reductase	65085	17461
b1154	1207501	1208130	<i>stfP</i>	e14 prophage; uncharacterized protein	1	8
b1156	1209119	1208517	<i>tfaE</i>	e14 prophage; putative tail fiber assembly protein	45	95
b1160	1212003	1211680	<i>iraM</i>	RpoS stabilizer during Mg starvation, anti-RssB factor	121	269
b1161	1213107	1212703	<i>ycgX</i>	DUF1398 family protein	24	183
b1162	1214059	1213328	<i>bluR</i>	repressor of blue light-responsive genes	1146	4644
b1163	1215475	1214264	<i>bluF</i>	anti-repressor for YcgE, blue light-responsive; FAD-binding; inactive c-di-GMP phosphodiesterase-like EAL domain protein	2017	2648
b1164	1215789	1216025	<i>ycgZ</i>	RcsB connector protein for regulation of biofilm and	56	3066

				acid-resistance		
b1165	1216068	1216340	<i>ymgA</i>	RcsB connector protein for regulation of biofilm	89	5284
b1166	1216369	1216635	<i>ariR</i>	RcsB connector protein for regulation of biofilm and acid-resistance	93	3840
b1167	1216748	1216996	<i>ymgC</i>	Blue light, low temperature and stress induced protein	15	1618
b1168	1217328	1218851	<i>ycgG</i>	putative membrane-anchored cyclic-di-GMP phosphodiesterase	68	1119
b1171	1222634	1222305	<i>ymgD</i>	uncharacterized protein	1348	570
b1172	1222988	1222644	<i>ymgG</i>	UPF0757 family protein	1736	148
b1174	1224545	1224279	<i>minE</i>	cell division topological specificity factor	3050	1915
b1175	1225361	1224549	<i>minD</i>	inhibitor of FtsZ ring polymerization; chromosome-membrane tethering protein; membrane ATPase of the MinCDEE system	11038	2700
b1176	1226080	1225385	<i>minC</i>	inhibitor of FtsZ ring polymerization	3507	2672
b1177	1226600	1226968	<i>ycgJ</i>	uncharacterized protein	354	333
b1178	1227472	1227071	<i>pliG</i>	periplasmic inhibitor of g-type lysozyme	279	449
b1179	1227714	1228007	<i>ycgL</i>	UPF0745 family protein	791	724
b1180	1228079	1228738	<i>ycgM</i>	putative isomerase/hydrolase	887	677
b1181	1228815	1229276	<i>ycgN</i>	UPF0153 family cysteine cluster protein	287	1001
b1182	1230394	1229483	<i>hlyE</i>	hemolysin E	490	332
b1183	1230767	1231186	<i>umuD</i>	translesion error-prone DNA polymerase V subunit; RecA-activated auto-protease	73	202
b1184	1231186	1232454	<i>umuC</i>	translesion error-prone DNA polymerase V subunit; DNA polymerase activity	138	352
b1185	1233030	1232500	<i>dsbB</i>	oxidoreductase that catalyzes reoxidation of DsbA protein disulfide isomerase I	722	1194
b1186	1234717	1233176	<i>nhaB</i>	sodium:proton antiporter	1270	654
b1187	1234938	1235657	<i>fadR</i>	fatty acid metabolism regulon transcriptional regulator	3201	1162
b1188	1237241	1235709	<i>ycgB</i>	SpoVR family stationary phase protein	8649	7790
b1189	1237571	1238869	<i>dadA</i>	D-amino acid dehydrogenase	8720	1886
b1190	1238879	1239949	<i>dadX</i>	alanine racemase, catabolic, PLP-binding	4416	1214
b1191	1242071	1240335	<i>cvrA</i>	putative cation/proton antiporter	782	1667
b1192	1243080	1242166	<i>ldcA</i>	murein tetrapeptide carboxypeptidase; LD-carboxypeptidase A	314	622
b1193	1243180	1243791	<i>emtA</i>	lytic murein endotransglycosylase E	495	614
b1194	1244527	1243793	<i>ycgR</i>	flagellar velocity braking protein, c-di-GMP-regulated	1494	1902
b1195	1244728	1244982	<i>ymgE</i>	UPF0410 family putative inner membrane protein	571	391
b1196	1245160	1245600	<i>ycgY</i>	uncharacterized protein	70	260
b1197	1247376	1245679	<i>treA</i>	periplasmic trehalase	1164	1250
b1198	1249114	1247696	<i>dhaM</i>	putative dihydroxyacetone-specific PTS enzymes: HPr, EI components	2719	636
b1199	1249757	1249125	<i>dhaL</i>	dihydroxyacetone kinase, C-terminal domain	1658	252
b1200	1250838	1249768	<i>dhaK</i>	dihydroxyacetone kinase, PTS-dependent, dihydroxyacetone-binding subunit	3350	589
b1201	1251066	1252985	<i>dhaR</i>	dhaKLM operon transcription activator	277	742
b1202	1255952	1253085	<i>ycgV</i>	putative adhesin	638	1864
b1203	1257812	1256721	<i>ychF</i>	catalase inhibitor protein; ATPase, K+-dependent, ribosome-associated	4240	4273
b1204	1258513	1257929	<i>pth</i>	peptidyl-tRNA hydrolase	392	515
b1205	1258791	1259069	<i>ychH</i>	DUF2583 family putative inner membrane protein	33530	9247
b1206	1260803	1259124	<i>dauA</i>	C4-dicarboxylic acid transporter	538	871
b1207	1261875	1260928	<i>prs</i>	phosphoribosylpyrophosphate synthase	12222	3493
b1208	1262877	1262026	<i>ispE</i>	4-diphosphocytidyl-2-C-methylerythritol kinase	763	447
b1209	1263500	1262877	<i>lolB</i>	lipoprotein localization factor	688	456
b1210	1263714	1264970	<i>hemA</i>	glutamyl tRNA reductase	825	980
b1211	1265012	1266094	<i>prfA</i>	peptide chain release factor RF-1	1117	1111
b1212	1266094	1266927	<i>prmC</i>	RF-1 and RF-2 N5-glutamine methyltransferase	395	859

b1213	1266924	1267316	<i>ychQ</i>	SIRB family inner membrane protein	147	277
b1214	1267320	1268129	<i>ychA</i>	transglutaminase-like TPR-repeat protein	744	758
b1215	1268165	1269019	<i>kdsA</i>	3-deoxy-D-manno-octulosonate 8-phosphate synthase	7299	1593
b1216	1271849	1270749	<i>chaA</i>	calcium/sodium:proton antiporter	201	1096
b1217	1272119	1272349	<i>chaB</i>	cation transport regulator	59	166
b1218	1272507	1273202	<i>chaC</i>	cation transport regulator	125	688
b1219	1273599	1273246	<i>ychN</i>	putative sulfur relay protein	6091	1839
b1220	1273784	1275178	<i>ychO</i>	putative invasins	322	728
b1221	1275829	1275179	<i>narL</i>	response regulator in two-component regulatory system with NarX	1003	390
b1222	1277618	1275822	<i>narX</i>	sensory histidine kinase in two-component regulatory system with NarL	1109	779
b1223	1277957	1279348	<i>narK</i>	nitrate/nitrite transporter	1805	923
b1224	1279864	1283607	<i>narG</i>	nitrate reductase 1, alpha subunit	8781	1985
b1225	1283604	1285142	<i>narH</i>	nitrate reductase 1, beta (Fe-S) subunit	1870	456
b1226	1285139	1285849	<i>narJ</i>	molybdenum-cofactor-assembly chaperone delta subunit of nitrate reductase 1	526	112
b1227	1285849	1286526	<i>narI</i>	nitrate reductase 1, gamma (cytochrome b(NR)) subunit	504	156
b1229	1287176	1287087	<i>tpr</i>	protamine-like protein	8	59
b1232	1288624	1287782	<i>purU</i>	formyltetrahydrofolate hydrolase	1336	1170
b1233	1289132	1288674	<i>ychJ</i>	UPF0225 family protein	370	834
b1234	1289245	1290150	<i>rssA</i>	putative patatin-like family phospholipase	854	737
b1235	1290242	1291255	<i>rssB</i>	PcnB-degradosome interaction factor; response regulator	1384	1288
b1236	1291457	1292365	<i>galU</i>	glucose-1-phosphate uridylyltransferase	7154	2586
b1237	1292922	1292509	<i>hns</i>	global DNA-binding transcriptional dual regulator H-NS	35795	25974
b1238	1293527	1294144	<i>tdk</i>	thymidine kinase/deoxyuridine kinase	461	562
b1241	1298121	1295446	<i>adhE</i>	fused acetaldehyde-CoA dehydrogenase/iron-dependent alcohol dehydrogenase/pyruvate-formate lyase deactivase	102342	19435
b1242	1298598	1299245	<i>ychE</i>	UPF0056 family inner membrane protein	559	764
b1243	1301182	1302813	<i>oppA</i>	oligopeptide ABC transporter periplasmic binding protein	11921	27739
b1244	1302899	1303819	<i>oppB</i>	oligopeptide ABC transporter permease	873	1167
b1245	1303834	1304742	<i>oppC</i>	oligopeptide ABC transporter permease	815	1205
b1246	1304754	1305767	<i>oppD</i>	oligopeptide ABC transporter ATPase	1175	1181
b1247	1305764	1306768	<i>oppF</i>	oligopeptide ABC transporter ATPase	1923	1731
b1248	1307150	1306821	<i>yciU</i>	UPF0263 family protein	526	733
b1249	1308645	1307185	<i>clsA</i>	cardiolipin synthase 1	1130	1288
b1250	1310269	1309016	<i>kch</i>	voltage-gated potassium channel	576	1636
b1251	1310865	1310569	<i>yciI</i>	putative DGPF domain-containing enzyme	1319	892
b1252	1311089	1311808	<i>tonB</i>	membrane spanning protein in TonB-ExbB-ExbD transport complex	2301	996
b1253	1312246	1311848	<i>yciA</i>	acyl-CoA esterase	380	610
b1254	1312890	1312351	<i>yciB</i>	IspA family inner membrane protein	508	675
b1255	1313663	1312920	<i>yciC</i>	UPF0259 family inner membrane protein	615	690
b1256	1314020	1314658	<i>ompW</i>	outer membrane protein W	12472	1320
b1257	1315224	1314718	<i>yciE</i>	putative rubrerythrin/ferritin-like metal-binding protein	234	626
b1258	1315770	1315270	<i>yciF</i>	putative rubrerythrin/ferritin-like metal-binding protein	86	724
b1259	1316035	1315856	<i>yciG</i>	KGG family protein	58	550
b1260	1317222	1316416	<i>trpA</i>	tryptophan synthase, alpha subunit	1269	4156
b1261	1318415	1317222	<i>trpB</i>	tryptophan synthase, beta subunit	1556	5349
b1262	1319788	1318427	<i>trpC</i>	indole-3-glycerolphosphate synthetase and N-(5-phosphoribosyl)anthranilate isomerase	501	4068
b1263	1321384	1319789	<i>trpD</i>	fused glutamine amidotransferase (component II) of anthranilate synthase/anthranilate phosphoribosyl transferase	184	4537
b1264	1322946	1321384	<i>trpE</i>	component I of anthranilate synthase	102	8705
b1266	1323220	1324101	<i>yciV</i>	PHP domain protein	823	929

b1267	1324098	1324718	<i>yciO</i>	putative RNA binding protein	1555	921
b1268	1324746	1326641	<i>yciQ</i>	enhancer of membrane protein expression; putative inner membrane protein	280	1582
b1269	1326852	1327727	<i>rluB</i>	23S rRNA pseudouridine(2605) synthase	938	777
b1270	1328357	1327767	<i>btuR</i>	cob(I)yrinic acid a,c-diamide adenosyltransferase	793	798
b1271	1329112	1328354	<i>yciK</i>	putative EmrKY-TolC system oxoacyl-(acyl carrier protein) reductase	1398	1064
b1272	1329332	1330381	<i>sohB</i>	inner membrane protein, S49 peptidase family protein	3088	2154
b1273	1330668	1330417	<i>yciN</i>	DUF2498 protein YciN	2181	2524
b1274	1331048	1333645	<i>topA</i>	DNA topoisomerase I, omega subunit	9549	9549
b1275	1333855	1334829	<i>cysB</i>	N-acetylserine-responsive cysteine regulon transcriptional activator; autorepressor	4809	11908
b1276	1335831	1338506	<i>acnA</i>	aconitate hydratase I; aconitase A	4250	3366
b1277	1339160	1338570	<i>ribA</i>	GTP cyclohydrolase II	2151	4062
b1278	1339330	1340094	<i>pgpB</i>	phosphatidylglycerophosphatase B	491	1179
b1279	1340243	1340551	<i>yciS</i>	DUF1049 family inner membrane protein, function unknown	1406	1962
b1280	1340558	1341727	<i>yciM</i>	LPS regulatory protein; putative modulator of LpxC proteolysis	1053	1407
b1281	1341921	1342658	<i>pyrF</i>	orotidine-5'-phosphate decarboxylase	574	545
b1282	1342658	1342984	<i>yciH</i>	initiation factor function partial mimic, SUI1 family	452	691
b1283	1343328	1343110	<i>osmB</i>	osmotically and stress inducible lipoprotein	2740	1372
b1284	1344346	1343597	<i>yciT</i>	global regulator of transcription; DeoR family	443	1838
b1285	1346742	1344757	<i>gmr</i>	cyclic-di-GMP phosphodiesterase; csgD regulator; modulator of RNase II stability	799	1446
b1286	1348912	1346978	<i>rnb</i>	ribonuclease II	4263	3450
b1287	1350107	1348980	<i>yciW</i>	putative oxidoreductase	889	1162
b1288	1351039	1350251	<i>fabI</i>	enoyl-[acyl-carrier-protein] reductase, NADH-dependent	14419	4708
b1289	1351760	1351407	<i>ycjD</i>	DUF559 family endonuclease-related protein	149	343
b1290	1352634	1351828	<i>sapF</i>	antimicrobial peptide ABC transporter ATPase	338	343
b1291	1353628	1352636	<i>sapD</i>	antimicrobial peptide ABC transporter ATPase	477	515
b1292	1354518	1353628	<i>sapC</i>	antimicrobial peptide transport ABC transporter permease	118	218
b1293	1355470	1354505	<i>sapB</i>	antimicrobial peptide transport ABC transporter permease	173	341
b1294	1357110	1355467	<i>sapA</i>	antimicrobial peptide transport ABC transporter periplasmic binding protein	571	825
b1295	1357668	1357423	<i>ymjA</i>	DUF2543 family protein	73	252
b1296	1359187	1357802	<i>puuP</i>	putrescine importer	243	604
b1297	1360908	1359490	<i>puuA</i>	glutamate--putrescine ligase	1086	1261
b1298	1361120	1361884	<i>puuD</i>	gamma-glutamyl-gamma-aminobutyrate hydrolase	832	1055
b1299	1361911	1362468	<i>puuR</i>	repressor for the divergent puu operons, putrescine inducible	902	808
b1300	1362743	1364230	<i>puuC</i>	gamma-glutamyl-gamma-aminobutyraldehyde dehydrogenase; succinate semialdehyde dehydrogenase	724	547
b1301	1364232	1365512	<i>puuB</i>	gamma-glutamylputrescine oxidoreductase	311	200
b1302	1365550	1366815	<i>puuE</i>	4-aminobutyrate aminotransferase, PLP-dependent	331	319
b1303	1367912	1366935	<i>pspF</i>	psp operon transcriptional activator	281	266
b1304	1368079	1368747	<i>pspA</i>	regulatory protein for phage-shock-protein operon	2754	153274
b1305	1368801	1369025	<i>pspB</i>	psp operon transcription co-activator	95	3819
b1306	1369025	1369384	<i>pspC</i>	psp operon transcription co-activator	125	2762
b1307	1369393	1369614	<i>pspD</i>	peripheral inner membrane phage-shock protein	30	644
b1308	1369689	1370003	<i>pspE</i>	thiosulfate:cyanide sulfurtransferase (rhodanese)	5823	6131
b1309	1370216	1371895	<i>ycjM</i>	alpha amylase catalytic domain family protein	180	681
b1310	1371909	1373201	<i>ycjN</i>	putative ABC sugar transporter periplasmic binding protein	106	91
b1311	1373222	1374103	<i>ycjO</i>	putative sugar ABC transporter permease	22	48
b1312	1374090	1374932	<i>ycjP</i>	putative sugar ABC transporter permease	17	92
b1313	1374963	1376015	<i>ycjQ</i>	putative Zn-dependent NAD(P)-binding oxidoreductase	51	42

b1314	1376034	1376822	<i>ycjR</i>	putative TIM alpha/beta barrel enzyme	46	49
b1315	1376832	1377887	<i>ycjS</i>	putative NADH-binding oxidoreductase	42	96
b1316	1377884	1380151	<i>ycjT</i>	putative family 65 glycosyl hydrolase	50	252
b1317	1380148	1380807	<i>ycjU</i>	beta-phosphoglucomutase	19	26
b1319	1381947	1382852	<i>ompG</i>	outer membrane porin G	5	183
b1320	1383961	1382963	<i>ycjW</i>	LacI family putative transcriptional repressor	198	276
b1321	1384117	1385514	<i>ycjX</i>	DUF463 family protein, putative P-loop NTPase	1560	950
b1322	1385511	1386572	<i>ycjF</i>	UPF0283 family inner membrane protein	982	695
b1323	1386720	1388261	<i>tyrR</i>	aromatic amino acid biosynthesis and transport regulon transcriptional regulator; autorepressor; ATPase; phosphatase	4212	2273
b1324	1388811	1388305	<i>tpx</i>	lipid hydroperoxide peroxidase	15111	4196
b1325	1388930	1389895	<i>ycjG</i>	L-Ala-D/L-Glu epimerase	632	1000
b1326	1390598	1389870	<i>mpaA</i>	murein peptide amidase A	990	793
b1327	1391853	1390933	<i>ycjY</i>	S9 homolog non-peptidase family protein	110	239
b1328	1391991	1392890	<i>pgrR</i>	murein peptide degradation regulator	189	489
b1329	1393227	1394840	<i>mppA</i>	murein tripeptide (L-ala-gamma-D-glutamyl-meso-DAP) transporter subunit	4074	1551
b1330	1395922	1394891	<i>ynaI</i>	mechanosensitive channel protein, very small conductance	489	709
b1331	1396076	1397092	<i>insH1</i>	IS5 transposase and trans-activator	3143	2558
b1332	1397365	1397622	<i>ynaJ</i>	DUF2534 family putative inner membrane protein	5845	7940
b1333	1398622	1397672	<i>uspE</i>	stress-induced protein	36399	13536
b1334	1399526	1398774	<i>fnr</i>	oxygen-sensing anaerobic growth regulon transcriptional regulator FNR; autorepressor	4105	9673
b1335	1400236	1399721	<i>ogt</i>	O-6-alkylguanine-DNA:cysteine-protein methyltransferase	117	241
b1336	1401773	1400247	<i>abgT</i>	p-aminobenzoyl-glutamate transporter; membrane protein	93	317
b1337	1403255	1401810	<i>abgB</i>	p-aminobenzoyl-glutamate hydrolase, B subunit	78	197
b1338	1404565	1403255	<i>abgA</i>	p-aminobenzoyl-glutamate hydrolase, A subunit	30	88
b1339	1404741	1405649	<i>abgR</i>	putative DNA-binding transcriptional regulator of abgABT operon	529	520
b1340	1405979	1406542	<i>smrA</i>	DNA endonuclease	245	1007
b1341	1407795	1406563	<i>ydaM</i>	diguanylate cyclase, csgD regulator	609	1686
b1342	1408050	1409033	<i>ydaN</i>	putative Zn(II) transporter	818	862
b1343	1409511	1410884	<i>dbpA</i>	ATP-dependent RNA helicase, specific for 23S rRNA	459	740
b1344	1411948	1411013	<i>ttaA</i>	tRNA s(2)C32 thioltransferase, iron sulfur cluster protein	1135	1143
b1345	1413235	1412000	<i>intR</i>	Rac prophage; integrase	146	1042
b1346	1413452	1413237	<i>ydaQ</i>	Rac prophage; conserved protein	2	25
b1347	1413740	1413531	<i>ydaC</i>	DUF1187 family protein, Rac prophage; putative double-strand break reduction protein	51	141
b1348	1413927	1413733	<i>ralR</i>	Rac prophage; restriction alleviation protein	8	101
b1349	1414793	1413984	<i>recT</i>	Rac prophage; recombination and repair protein	105	212
b1350	1417386	1414786	<i>recE</i>	Rac prophage; exonuclease VIII, 5' to 3' specific dsDNA exonuclease	210	983
b1351	1417763	1417488	<i>racC</i>	Rac prophage; uncharacterized protein	25	86
b1352	1418229	1418008	<i>kilR</i>	killing protein, Rac prophage; FtsZ inhibitor protein	9	158
b1353	1418671	1419159	<i>sieB</i>	phage superinfection exclusion protein, Rac prophage	35	317
b1355	1419456	1419322	<i>ydaG</i>	Rac prophage; uncharacterized protein	5	20
b1356	1420241	1419765	<i>racR</i>	Rac prophage; putative DNA-binding transcriptional regulator	1753	6337
b1357	1420365	1420661	<i>ydaS</i>	Rac prophage; putative DNA-binding transcriptional regulator	37	49
b1358	1420684	1421106	<i>ydaT</i>	Rac prophage; uncharacterized protein	49	42
b1359	1421119	1421976	<i>ydaU</i>	Rac prophage; conserved protein	114	201
b1360	1421983	1422729	<i>ydaV</i>	Rac prophage; putative DNA replication protein	34	50
b1363	1423782	1425239	<i>trkG</i>	Rac prophage; potassium transporter subunit	719	2211

b1365	1425377	1425640	<i>ynaK</i>	Rac prophage; conserved protein	15	94
b1370	1428726	1427746	<i>insH1</i>	IS5 transposase and trans-activator	1191	1714
b1372	1429049	1432411	<i>stfR</i>	Rac prophage; putative tail fiber protein	128	602
b1373	1432411	1432986	<i>tfaR</i>	Rac prophage; putative tail fiber assembly protein	40	134
b1374	1433674	1433084	<i>pinR</i>	Rac prophage; putative site-specific recombinase	129	1107
b1375	1434224	1433991	<i>ynaE</i>	cold shock protein, Rac prophage	62	3776
b1376	1435619	1435185	<i>uspF</i>	stress-induced protein, ATP-binding protein	19083	13592
b1377	1436893	1435760	<i>ompN</i>	outer membrane pore protein N, non-specific	32	210
b1378	1440784	1437260	<i>pfo</i>	pyruvate-flavodoxin oxidoreductase	6917	2848
b1379	1441743	1441321	<i>hslJ</i>	heat-inducible lipoprotein involved in novobiocin resistance	1890	1264
b1380	1442843	1441854	<i>ldhA</i>	fermentative D-lactate dehydrogenase, NAD-dependent	1134	649
b1381	1443051	1445690	<i>ydbH</i>	putative membrane-anchored protein, function unknown	635	1293
b1382	1445687	1445872	<i>ynbE</i>	lipoprotein	47	78
b1383	1445880	1446206	<i>ydbL</i>	DUF1318 family protein	192	570
b1384	1447283	1446378	<i>feaR</i>	transcriptional activator for <i>tynA</i> and <i>feaB</i>	1699	1347
b1385	1447519	1449018	<i>feaB</i>	phenylacetaldehyde dehydrogenase	470	900
b1386	1451349	1449076	<i>tynA</i>	tyramine oxidase, copper-requiring	128	959
b1387	1453642	1451597	<i>paaZ</i>	oxepin-CoA hydrolase and 3-oxo-5,6-dehydrosuberyl-CoA semialdehyde dehydrogenase	54	174
b1388	1453927	1454856	<i>paaA</i>	ring 1,2-phenylacetyl-CoA epoxidase subunit	86	141
b1389	1454868	1455155	<i>paaB</i>	putative ring 1,2-phenylacetyl-CoA epoxidase subunit	22	23
b1390	1455164	1455910	<i>paaC</i>	ring 1,2-phenylacetyl-CoA epoxidase subunit	46	41
b1391	1455925	1456422	<i>paaD</i>	ring 1,2-phenylacetyl-CoA epoxidase subunit	26	34
b1392	1456430	1457500	<i>paaE</i>	ring 1,2-phenylacetyl-CoA epoxidase, NAD(P)H oxidoreductase component	52	80
b1393	1457497	1458264	<i>paaF</i>	2,3-dehydroadipyl-CoA hydratase	26	87
b1394	1458264	1459052	<i>paaG</i>	1,2-epoxyphenylacetyl-CoA isomerase, oxepin-CoA-forming	18	40
b1395	1459054	1460481	<i>paaH</i>	3-hydroxyadipyl-CoA dehydrogenase, NAD ⁺ -dependent	43	402
b1396	1460471	1460893	<i>paaI</i>	hydroxyphenylacetyl-CoA thioesterase	21	17
b1397	1460893	1462098	<i>paaJ</i>	3-oxoadipyl-CoA/3-oxo-5,6-dehydrosuberyl-CoA thiolase	2417	467
b1398	1462125	1463438	<i>paaK</i>	phenylacetyl-CoA ligase	2245	580
b1399	1463539	1464489	<i>paaX</i>	transcriptional repressor of phenylacetic acid degradation <i>paa</i> operon, phenylacetyl-CoA inducer	511	497
b1400	1464471	1465061	<i>paaY</i>	thioesterase required for phenylacetic acid degradation; trimeric; phenylacetate regulatory and detoxification protein; hexapeptide repeat protein	447	463
b1402	1468826	1467921	<i>insD1</i>	IS2 transposase TnpB	652	819
b1403	1469149	1468784	<i>insC1</i>	IS2 repressor TnpA	403	429
b1404	1469358	1470509	<i>insI1</i>	IS30 transposase	629	1322
b1406	1474221	1475081	<i>ydbC</i>	putative NAD(P)-binding oxidoreductase	3248	461
b1407	1475144	1477450	<i>ydbD</i>	PF10971 family putative periplasmic methylglyoxal resistance protein	129	1262
b1408	1477621	1478226	<i>ynbA</i>	inner membrane protein	3	93
b1409	1478226	1479122	<i>ynbB</i>	putative CDP-diglyceride synthase	6	637
b1410	1479138	1480895	<i>ynbC</i>	putative esterase	68	294
b1411	1480909	1482201	<i>ynbD</i>	putative phosphatase inner membrane protein	125	648
b1412	1482860	1482255	<i>azoR</i>	NADH-azoreductase, FMN-dependent	582	187
b1413	1483061	1486963	<i>hrpA</i>	putative ATP-dependent helicase	2422	2813
b1414	1487235	1488035	<i>ycdF</i>	DUF218 superfamily protein, SAM-binding	2804	1915
b1415	1488232	1489671	<i>aldA</i>	aldehyde dehydrogenase A, NAD-linked	46928	25805
b1418	1490902	1491432	<i>cybB</i>	cytochrome b561	2094	1400
b1419	1491677	1491850	<i>ycdA</i>	putative periplasmic protein	254	245
b1420	1492129	1491962	<i>mokB</i>	regulatory peptide	426	2898
b1421	1492470	1494110	<i>trg</i>	methyl-accepting chemotaxis protein III, ribose and	2268	2474

				galactose sensor receptor		
b1422	1495071	1494148	<i>ycdI</i>	putative DNA-binding transcriptional regulator	3434	2234
b1423	1495288	1496631	<i>ycdJ</i>	putative metalloenzyme	6061	1056
b1424	1496856	1498511	<i>opgD</i>	OPG biosynthetic periplasmic protein	4177	3314
b1426	1498651	1498875	<i>ycdH</i>	DUF465 family protein	12820	6081
b1427	1498938	1499477	<i>rimL</i>	ribosomal-protein-L7/L12-serine acetyltransferase	2010	1246
b1428	1500449	1499469	<i>ycdK</i>	uncharacterized protein	351	927
b1429	1500573	1501565	<i>tehA</i>	potassium-tellurite ethidium and proflavin transporter	283	452
b1430	1501562	1502155	<i>tehB</i>	tellurite, selenium methyltransferase, SAM-dependent; tellurite, selenium resistance protein	515	681
b1431	1502457	1503125	<i>ycdL</i>	lipoprotein	2732	5275
b1432	1503717	1504865	<i>insQ</i>	IS609 transposase B	789	1377
b1433	1506080	1504905	<i>ycdO</i>	BenE family inner membrane putative transporter	565	878
b1434	1506172	1506708	<i>ycdN</i>	putative DNA-binding transcriptional regulator	170	223
b1435	1506781	1508742	<i>ycdP</i>	putative peptidase	1005	1446
b1436	1509064	1508834	<i>yncJ</i>	uncharacterized protein	11	1528
b1438	1509508	1509924	<i>hicB</i>	antitoxin for the HicAB toxin-antitoxin system	416	476
b1439	1510003	1511409	<i>ycdR</i>	putative DNA-binding transcriptional regulator and putative aminotransferase	520	750
b1440	1511654	1512799	<i>ycdS</i>	putative ABC transporter periplasmic binding protein	4347	1364
b1441	1512817	1513830	<i>ycdT</i>	putative ABC transporter ATPase	797	255
b1442	1513831	1514772	<i>ycdU</i>	putative ABC transporter permease	242	282
b1443	1514762	1515556	<i>ycdV</i>	putative ABC transporter permease	272	135
b1444	1515578	1517002	<i>patD</i>	gamma-aminobutyraldehyde dehydrogenase	1310	683
b1445	1517389	1517562	<i>ycdX</i>	DUF2566 family protein	30	144
b1446	1517648	1517881	<i>ycdY</i>	DUF2526 family protein	1062	2300
b1447	1518331	1517882	<i>ycdZ</i>	DUF606 family inner membrane protein	112	641
b1448	1518846	1518328	<i>mnaT</i>	methionine N-acyltransferase; L-amino acid N-acyltransferase	368	626
b1449	1519027	1520064	<i>curA</i>	curcumin/dihydrocurcumin reductase, NADPH-dependent	1143	883
b1450	1520262	1520927	<i>mcbR</i>	colanic acid and biofilm gene transcriptional regulator, MqsR-controlled	169	464
b1451	1523065	1520963	<i>yncD</i>	putative iron outer membrane transporter	917	1142
b1452	1523307	1524368	<i>yncE</i>	ATP-binding protein, periplasmic, function unknown	4373	1408
b1453	1525980	1524481	<i>ansP</i>	L-asparagine transporter	171	467
b1454	1526247	1526864	<i>yncG</i>	glutathione S-transferase homolog	73	436
b1455	1526940	1527152	<i>yncH</i>	IPR020099 family protein	1	44
b1457	1529922	1530404	<i>ycdD</i>	putative immunity protein for RhsE	92	1280
b1460	1531816	1532952	<i>ycdC</i>	H repeat-associated putative transposase	53	1364
b1461	1533052	1533285	<i>pptA</i>	4-oxalocrotonate tautomerase	83	117
b1462	1533851	1533282	<i>yddH</i>	flavin reductase like-protein	424	351
b1463	1534024	1534869	<i>nhoA</i>	N-hydroxyarylamine O-acetyltransferase	83	218
b1464	1535858	1534965	<i>yddE</i>	PhzC-PhzF family protein	931	678
b1465	1536617	1535937	<i>narV</i>	nitrate reductase 2 (NRZ), gamma subunit	44	94
b1466	1537309	1536614	<i>narW</i>	nitrate reductase 2 (NRZ), delta subunit (assembly subunit)	52	91
b1467	1538853	1537309	<i>narY</i>	nitrate reductase 2 (NRZ), beta subunit	126	294
b1468	1542590	1538850	<i>narZ</i>	nitrate reductase 2 (NRZ), alpha subunit	383	1019
b1469	1544060	1542672	<i>narU</i>	nitrate/nitrite transporter	100	699
b1473	1547169	1546288	<i>yddG</i>	aromatic amino acid exporter	207	222
b1474	1547401	1550448	<i>fdnG</i>	formate dehydrogenase-N, alpha subunit, nitrate-inducible	2071	513
b1475	1550461	1551345	<i>fdnH</i>	formate dehydrogenase-N, Fe-S (beta) subunit, nitrate-inducible	310	164
b1476	1551338	1551991	<i>fdnI</i>	formate dehydrogenase-N, cytochrome B556 (gamma) subunit, nitrate-inducible	315	402

b1477	1552682	1552398	<i>yddM</i>	putative DNA-binding transcriptional regulator	142	285
b1478	1553838	1552828	<i>adhP</i>	ethanol-active dehydrogenase/acetaldehyde-active reductase	1065	677
b1479	1555669	1553972	<i>maeA</i>	malate dehydrogenase, decarboxylating, NAD-requiring; malic enzyme	12304	2881
b1480	1555963	1555826	<i>sra</i>	stationary-phase-induced ribosome-associated protein	7535	25286
b1481	1556280	1556065	<i>bdm</i>	biofilm-dependent modulation protein	31	124
b1482	1556625	1557056	<i>osmC</i>	lipoyl-dependent Cys-based peroxidase, hydroperoxide resistance; salt-shock inducible membrane protein; peroxiredoxin	2139	3233
b1483	1558038	1557112	<i>ddpF</i>	D,D-dipeptide ABC transporter ATPase	125	204
b1484	1559017	1558031	<i>ddpD</i>	D,D-dipeptide ABC transporter ATPase	72	78
b1485	1559910	1559014	<i>ddpC</i>	D,D-dipeptide ABC transporter permease	116	222
b1486	1560929	1559907	<i>ddpB</i>	D,D-dipeptide ABC transporter permease	80	140
b1487	1562481	1560931	<i>ddpA</i>	D,D-dipeptide ABC transporter periplasmic binding protein	993	633
b1488	1563076	1562495	<i>ddpX</i>	D-ala-D-ala dipeptidase, Zn-dependent	406	153
b1489	1565733	1563334	<i>dosP</i>	oxygen sensor, c-di-GMP phosphodiesterase, heme-regulated; cold- and stationary phase-induced biofilm regulator	992	1655
b1490	1567140	1565758	<i>dosC</i>	diguanylate cyclase, cold- and stationary phase-induced oxygen-dependent biofilm regulator	2327	5037
b1491	1568823	1567504	<i>yddW</i>	liprotein, glycosyl hydrolase homolog	954	841
b1492	1570489	1568954	<i>gadC</i>	glutamate:gamma-aminobutyric acid antiporter	201	605
b1493	1572045	1570645	<i>gadB</i>	glutamate decarboxylase B, PLP-dependent	93	158
b1494	1575202	1572407	<i>pqqL</i>	putative periplasmic M16 family zinc metalloendopeptidase	513	711
b1495	1577619	1575247	<i>yddB</i>	putative TonB-dependent outer membrane receptor	279	640
b1496	1579342	1577657	<i>yddA</i>	putative multidrug ABC transporter permease/ATPase	47	288
b1497	1580790	1579633	<i>ydeM</i>	putative YdeN-specific sulfatase-maturing enzyme	666	204
b1498	1582524	1580842	<i>ydeN</i>	putative Ser-type periplasmic non-aryl sulfatase	9453	1495
b1499	1583687	1582926	<i>ydeO</i>	UV-inducible global regulator, EvgA-, GadE-dependent	19	241
b1500	1583959	1583762	<i>safA</i>	two-component system connector membrane protein, EvgSA to PhoQP	0	33
b1501	1586486	1584207	<i>ydeP</i>	putative oxidoreductase	234	528
b1502	1587734	1586820	<i>ydeQ</i>	putative fimbrial-like adhesin protein	9	243
b1503	1588296	1587793	<i>ydeR</i>	putative fimbrial-like adhesin protein	5	155
b1504	1588839	1588309	<i>ydeS</i>	putative fimbrial-like adhesin protein	5	670
b1507	1592176	1590854	<i>hipA</i>	inactivating GltX kinase facilitating persister formation; toxin of HipAB TA pair; autokinase	2069	1272
b1508	1592442	1592176	<i>hipB</i>	antitoxin of HipAB toxin-antitoxin system	741	548
b1511	1600209	1598617	<i>lsrK</i>	autoinducer-2 (AI-2) kinase	1158	762
b1512	1601241	1600288	<i>lsrR</i>	Lsr operon transcriptional repressor	1453	535
b1513	1601490	1603025	<i>lsrA</i>	autoinducer 2 import ATP-binding protein	775	141
b1514	1603019	1604047	<i>lsrC</i>	autoinducer 2 import system permease protein	147	126
b1515	1604047	1605039	<i>lsrD</i>	autoinducer 2 import system permease protein	86	133
b1516	1605051	1606073	<i>lsrB</i>	autoinducer 2-binding protein	333	416
b1517	1606100	1606975	<i>lsrF</i>	putative autoinducer-2 (AI-2) aldolase	315	108
b1518	1606999	1607289	<i>lsrG</i>	autoinducer-2 (AI-2) degrading protein LsrG	106	70
b1519	1607346	1608104	<i>tam</i>	trans-aconitate methyltransferase	652	676
b1520	1609022	1608108	<i>yneE</i>	bestrophin family putative inner membrane protein	219	665
b1521	1610680	1609229	<i>uxaB</i>	altronate oxidoreductase, NAD-dependent	810	773
b1522	1611854	1610907	<i>yneF</i>	putative membrane-bound diguanylate cyclase	86	299
b1523	1612325	1611966	<i>yneG</i>	DUF4186 family protein	171	847
b1524	1613251	1612325	<i>glsB</i>	glutaminase 2	269	285
b1525	1614703	1613315	<i>sad</i>	succinate semialdehyde dehydrogenase, NAD(P)+-dependent	1301	432
b1526	1614804	1615685	<i>yneJ</i>	putative DNA-binding transcriptional regulator	227	157

b1527	1615763	1616878	<i>yneK</i>	uncharacterized protein	24	587
b1528	1617028	1618218	<i>ydeA</i>	arabinose efflux transporter, arabinose-inducible	171	716
b1529	1618908	1618243	<i>marC</i>	UPF0056 family inner membrane protein	636	413
b1530	1619120	1619554	<i>marR</i>	transcriptional repressor of multiple antibiotic resistance	90	941
b1531	1619574	1619957	<i>marA</i>	multiple antibiotic resistance transcriptional regulator	493	3712
b1532	1619989	1620207	<i>marB</i>	periplasmic mar operon regulator	49	98
b1533	1621137	1620238	<i>eamA</i>	cysteine and O-acetyl-L-serine efflux system	592	982
b1534	1621332	1622519	<i>ydeE</i>	putative transporter	258	494
b1535	1623850	1622960	<i>dgcZ</i>	diguanylate cyclase, zinc-sensing	618	7466
b1536	1624497	1624105	<i>ydeI</i>	hydrogen peroxide resistance OB fold protein; putative periplasmic protein	531	1137
b1537	1624773	1625291	<i>ydeJ</i>	inactive PncC family protein	111	362
b1538	1627380	1625335	<i>dcp</i>	dipeptidyl carboxypeptidase II	3262	1772
b1539	1627517	1628263	<i>ydfG</i>	NADP-dependent 3-hydroxy acid dehydrogenase; malonic semialdehyde reductase	6166	2037
b1540	1628352	1629038	<i>rspR</i>	transcriptional repressor for <i>rspAB</i>	813	1196
b1541	1629215	1629418	<i>ydfZ</i>	selenoprotein, function unknown	232	606
b1542	1630913	1629453	<i>ydfI</i>	putative NAD-dependent D-mannonate oxidoreductase	78	296
b1544	1633072	1633305	<i>ydfK</i>	cold shock protein, function unknown, Qin prophage	84	2956
b1545	1633622	1634212	<i>pinQ</i>	Qin prophage; putative site-specific recombinase	124	1217
b1546	1634885	1634310	<i>tfaQ</i>	Qin prophage; putative tail fibre assembly protein	34	338
b1547	1635847	1634885	<i>stfQ</i>	Qin prophage; putative side tail fibre assembly protein	18	104
b1549	1637047	1637457	<i>ydfO</i>	Qin prophage; uncharacterized protein	120	441
b1550	1637782	1637609	<i>gnsB</i>	Qin prophage; multicopy suppressor of <i>secG</i> (Cs) and <i>fabA6</i> (Ts)	2351	15409
b1551	1638109	1637954	<i>ynfN</i>	Qin prophage; cold shock-induced protein	1	42
b1552	1638667	1638455	<i>cspI</i>	Qin prophage; cold shock protein	42	1237
b1553	1639527	1639030	<i>rzpQ</i>	Rz-like protein, Qin prophage	12	230
b1554	1640057	1639524	<i>rrrQ</i>	Qin prophage; putative lysozyme	21	86
b1555	1640365	1640054	<i>ydfR</i>	Qin prophage; uncharacterized protein	17	105
b1556	1640585	1640370	<i>essQ</i>	Qin prophage; putative S lysis protein	9	30
b1557	1641554	1641339	<i>cspB</i>	Qin prophage; cold shock protein	271	798
b1558	1641855	1642067	<i>cspF</i>	Qin prophage; cold shock protein	33	231
b1559	1643241	1642489	<i>quuQ</i>	Qin prophage; putative antitermination protein Q	50	357
b1560	1644304	1643255	<i>ydfU</i>	Qin prophage; uncharacterized protein	23	101
b1561	1644902	1644651	<i>rem</i>	Qin prophage; uncharacterized protein	53	367
b1562	1645274	1645119	<i>hokD</i>	Qin prophage; small toxic polypeptide	423	394
b1563	1645633	1645346	<i>relE</i>	Qin prophage; toxin of the RelE-RelB toxin-antitoxin system	384	922
b1564	1645872	1645633	<i>relB</i>	antitoxin of the RelE-RelB toxin-antitoxin system; transcriptional repressor	173	544
b1565	1645897	1646202	<i>ydfV</i>	Qin prophage; uncharacterized protein	40	184
b1566	1646405	1646737	<i>flxA</i>	Qin prophage; uncharacterized protein	1672	11487
b1569	1647850	1647620	<i>dicC</i>	Qin prophage; DNA-binding transcriptional regulator for DicB	4	39
b1570	1647934	1648341	<i>dicA</i>	Qin prophage; putative regulator for DicB	1599	6135
b1571	1648508	1648663	<i>ydfA</i>	Qin prophage; uncharacterized protein	3	20
b1572	1648665	1648793	<i>ydfB</i>	Qin prophage; uncharacterized protein	2	9
b1573	1648823	1649041	<i>ydfC</i>	uncharacterized protein, Qin prophage	23	77
b1575	1649609	1649797	<i>dicB</i>	Qin prophage; cell division inhibition protein	5	118
b1576	1649794	1649985	<i>ydfD</i>	Qin prophage; uncharacterized protein	0	16
b1580	1653915	1652896	<i>rspB</i>	putative Zn-dependent NAD(P)-binding oxidoreductase	70	2070
b1581	1655141	1653927	<i>rspA</i>	bifunctional D-altronate/D-mannonate dehydratase	72	239
b1582	1655673	1655347	<i>ynfA</i>	UPF0060 family inner membrane protein	88	253
b1583	1655808	1656149	<i>ynfB</i>	UPF0482 family putative periplasmic protein	1335	2394

b1584	1656184	1656744	<i>speG</i>	spermidine N(1)-acetyltransferase	711	1295
b1585	1657457	1656747	<i>ynfC</i>	UPF0257 family lipoprotein	598	1335
b1586	1657565	1657870	<i>ynfD</i>	DUF1161 family periplasmic protein	669	1517
b1587	1658069	1660495	<i>ynfE</i>	putative selenate reductase, periplasmic	2089	884
b1588	1660556	1662979	<i>ynfF</i>	S- and N-oxide reductase, A subunit, periplasmic	1782	1016
b1589	1662990	1663607	<i>ynfG</i>	oxidoreductase, Fe-S subunit	289	166
b1590	1663609	1664463	<i>ynfH</i>	oxidoreductase, membrane subunit	381	279
b1591	1664506	1665120	<i>dmsD</i>	twin-arginine leader-binding protein for DmsA and TorA	379	265
b1592	1665315	1666571	<i>clcB</i>	H(+)/Cl(-) exchange transporter	68	407
b1593	1667219	1666524	<i>ynfK</i>	putative dethiobiotin synthetase	2298	5430
b1594	1668564	1667344	<i>mlc</i>	glucosamine anaerobic growth regulon transcriptional repressor; autorepressor	5064	2733
b1595	1669592	1668699	<i>ynfL</i>	LysR family putative transcriptional regulator	74	155
b1596	1669699	1670952	<i>ynfM</i>	putative arabinose efflux transporter	629	2293
b1597	1671376	1671684	<i>asr</i>	acid shock-inducible periplasmic protein	687	1213
b1598	1671960	1672781	<i>ydgD</i>	putative peptidase	1603	1654
b1599	1673149	1672820	<i>mdtI</i>	multidrug efflux system transporter	31	92
b1600	1673501	1673136	<i>mdtJ</i>	multidrug efflux system transporter	59	360
b1601	1673913	1674947	<i>tqsA</i>	pheromone AI-2 transporter	361	995
b1602	1676360	1674972	<i>pntB</i>	pyridine nucleotide transhydrogenase, beta subunit	3072	1214
b1603	1677903	1676371	<i>pntA</i>	pyridine nucleotide transhydrogenase, alpha subunit	5986	1867
b1604	1678427	1679371	<i>ydgH</i>	DUF1471 family periplasmic protein	5985	1661
b1605	1679557	1680939	<i>ydgI</i>	putative arginine/ornithine antiporter transporter	213	503
b1606	1680976	1681698	<i>folM</i>	dihydromonapterin reductase, NADPH-dependent; dihydrofolate reductase isozyme	518	508
b1607	1682030	1681695	<i>ydgC</i>	GlpM family inner membrane protein	181	457
b1608	1682159	1682878	<i>rstA</i>	response regulator of RstAB two-component system	773	3149
b1609	1682882	1684183	<i>rstB</i>	sensory histidine kinase of RstAB two-component system	793	1725
b1610	1684259	1685188	<i>tus</i>	inhibitor of replication at Ter, DNA-binding protein	959	1166
b1611	1686588	1685185	<i>fumC</i>	fumarate hydratase (fumarase C), aerobic Class II	11914	2336
b1612	1688377	1686731	<i>fumA</i>	fumarate hydratase (fumarase A), aerobic Class I	56392	5365
b1613	1688576	1689751	<i>manA</i>	mannose-6-phosphate isomerase	4268	2000
b1614	1689852	1691360	<i>ydgA</i>	DUF945 family protein	11468	5515
b1615	1692851	1691586	<i>uidC</i>	putative outer membrane porin for beta-glucuronides porin protein	19	399
b1616	1694263	1692890	<i>uidB</i>	glucuronide transporter	33	210
b1617	1696071	1694260	<i>uidA</i>	beta-D-glucuronidase	152	311
b1618	1697052	1696462	<i>uidR</i>	transcriptional repressor	3091	4004
b1619	1698040	1697273	<i>hdhA</i>	7-alpha-hydroxysteroid dehydrogenase, NAD-dependent	2184	832
b1620	1699180	1698152	<i>mall</i>	transcriptional repressor of Mal regulon	1255	325
b1621	1699355	1700947	<i>malX</i>	maltose and glucose-specific PTS enzyme IIB component and IIC component	1562	554
b1622	1700957	1702129	<i>malY</i>	PLP-dependent beta-cystathionase and maltose regulon regulator	1108	751
b1623	1702233	1703234	<i>add</i>	adenosine deaminase	5721	1706
b1624	1704308	1703268	<i>ydgJ</i>	putative oxidoreductase	3517	2740
b1625	1704949	1705164	<i>cnu</i>	nucleoid-associated oriC-binding protein; H-NS and StpA stabilizing factor	38	122
b1626	1705250	1705690	<i>ydgK</i>	DUF2569 family inner membrane protein	572	829
b1627	1705767	1706348	<i>rsxA</i>	SoxR iron-sulfur cluster reduction factor component; inner membrane protein of electron transport complex	219	328
b1628	1706348	1706926	<i>rsxB</i>	SoxR iron-sulfur cluster reduction factor component; putative iron-sulfur protein	239	268
b1629	1706919	1709141	<i>rsxC</i>	SoxR iron-sulfur cluster reduction factor component; putative membrane-associated NADH oxidoreductase of electron transport complex	840	674

b1630	1709142	1710200	<i>rsxD</i>	SoxR iron-sulfur cluster reduction factor component; putative membrane protein of electron transport complex	572	290
b1631	1710204	1710824	<i>rsxG</i>	SoxR iron-sulfur cluster reduction factor component; putative membrane protein of electron transport complex	496	135
b1632	1710828	1711523	<i>rsxE</i>	SoxR iron-sulfur cluster reduction factor component; electron transport inner membrane NADH-quinone reductase	823	180
b1633	1711523	1712158	<i>nth</i>	DNA glycosylase and apyrimidinic (AP) lyase (endonuclease III)	587	161
b1634	1712769	1714271	<i>dtpA</i>	dipeptide and tripeptide permease A	5375	1733
b1635	1714377	1714982	<i>gstA</i>	glutathione S-transferase	2477	2343
b1636	1715889	1715026	<i>pdxY</i>	pyridoxamine kinase	1384	690
b1637	1717222	1715948	<i>tyrS</i>	tyrosyl-tRNA synthetase	8448	3360
b1638	1718007	1717351	<i>pdxH</i>	pyridoxine 5'-phosphate oxidase	1870	546
b1639	1718395	1718066	<i>mliC</i>	inhibitor of c-type lysozyme, membrane-bound; putative lipoprotein	593	327
b1640	1719602	1718493	<i>anmK</i>	anhydro-N-acetylmuramic acid kinase	1392	687
b1641	1719876	1720343	<i>slyB</i>	outer membrane lipoprotein	19323	10811
b1642	1720824	1720390	<i>slyA</i>	global transcriptional regulator	7238	7750
b1643	1721025	1721261	<i>ydhI</i>	DUF1656 family putative inner membrane efflux pump associated protein	139	486
b1644	1721264	1722121	<i>ydhJ</i>	putative membrane fusion protein (MFP) of YdhJK efflux pump	159	516
b1645	1722121	1724133	<i>ydhK</i>	putative efflux protein (PET) component of YdhJK efflux pump	273	835
b1646	1724655	1724134	<i>sodC</i>	superoxide dismutase, Cu, Zn, periplasmic	1384	2654
b1647	1725632	1724736	<i>ydhF</i>	putative oxidoreductase	7077	1040
b1648	1725920	1725681	<i>ydhL</i>	DUF1289 family protein	150	509
b1649	1726023	1726622	<i>nemR</i>	transcriptional repressor for the nemRA-gloA operon, quinone-, glyoxal-, and HOCl-activated	74	139
b1650	1726659	1727756	<i>nemA</i>	chromate reductase, quinone reductase, FMN-linked; N-Ethylmaleimide reductase; old yellow enzyme	1261	420
b1651	1727837	1728244	<i>gloA</i>	glyoxalase I, Ni-dependent	2533	1470
b1652	1728347	1728994	<i>rnt</i>	RNase T; exoribonuclease T; structured DNA 3' exonuclease; RNA processing; DNA repair	297	338
b1653	1729087	1733703	<i>lhr</i>	putative ATP-dependent helicase	548	992
b1654	1734101	1733754	<i>grxD</i>	glutaredoxin-4	4988	2659
b1655	1734435	1735250	<i>mepH</i>	murein DD-endopeptidase, space-maker hydrolase	1579	1667
b1656	1735378	1735959	<i>sodB</i>	superoxide dismutase, Fe	10902	3519
b1657	1737290	1736121	<i>ydhP</i>	putative MFS transporter, inner membrane protein	179	277
b1658	1737844	1738869	<i>purR</i>	transcriptional repressor, hypoxanthine-binding	1215	999
b1659	1739798	1738866	<i>ydhB</i>	LysR family putative transcriptional regulator	191	325
b1660	1739911	1741122	<i>ydhC</i>	putative arabinose efflux transporter	194	484
b1661	1741413	1742561	<i>cfa</i>	cyclopropane fatty acyl phospholipid synthase, SAM-dependent	5559	6168
b1662	1743242	1742601	<i>ribC</i>	riboflavin synthase, alpha subunit	2417	1899
b1663	1743457	1744830	<i>mdtK</i>	multidrug efflux system transporter	983	1100
b1664	1746127	1744871	<i>ydhQ</i>	autotransporter adhesin-related protein	7105	3853
b1667	1746700	1747005	<i>ydhR</i>	putative monooxygenase	2723	6911
b1668	1747131	1748735	<i>ydhS</i>	putative oxidoreductase	1291	2885
b1669	1749559	1748747	<i>ydhT</i>	FNR, Nar, NarP-regulated protein; putative subunit of YdhYVWXUT oxidoreductase complex	133	226
b1670	1750348	1749563	<i>ydhU</i>	putative cytochrome b subunit of YdhYVWXUT oxidoreductase complex	181	315
b1671	1751013	1750345	<i>ydhX</i>	putative 4Fe-4S ferridoxin-type protein; FNR, Nar, NarP-regulated protein; putative subunit of YdhYVWXUT oxidoreductase complex	219	191
b1672	1751724	1751077	<i>ydhW</i>	FNR, Nar, NarP-regulated protein; putative subunit of YdhYVWXUT oxidoreductase complex	219	178
b1673	1753830	1751728	<i>ydhV</i>	putative oxidoreductase subunit	2714	1036

b1674	1754477	1753851	<i>ydhY</i>	putative 4Fe-4S ferridoxin-type protein; FNR, Nar, NarP-regulated protein; putative subunit of YdhYVWXUT oxidoreductase complex	847	260
b1675	1755141	1754932	<i>ydhZ</i>	uncharacterized protein	147	793
b1676	1755698	1757110	<i>pykF</i>	pyruvate kinase I	28163	6824
b1677	1757421	1757657	<i>lpp</i>	murein lipoprotein	496427	83362
b1678	1758725	1757721	<i>ldtE</i>	murein L,D-transpeptidase	2128	2086
b1679	1759290	1758874	<i>sufE</i>	sulfur acceptor protein	341	225
b1680	1760523	1759303	<i>sufS</i>	cysteine desulfurase, stimulated by SufE; selenocysteine lyase, PLP-dependent	817	493
b1681	1761791	1760520	<i>sufD</i>	component of SufBCD Fe-S cluster assembly scaffold	1015	544
b1682	1762512	1761766	<i>sufC</i>	SufBCD Fe-S cluster assembly scaffold protein, ATP-binding protein	555	290
b1683	1764009	1762522	<i>sufB</i>	component of SufBCD Fe-S cluster assembly scaffold	1191	701
b1684	1764386	1764018	<i>sufA</i>	Fe-S cluster assembly protein	239	245
b1685	1765122	1764934	<i>ydiH</i>	uncharacterized protein	327	2379
b1686	1765632	1765222	<i>menI</i>	1,4-dihydroxy-2-naphthoyl-CoA hydrolase	593	514
b1687	1768685	1765629	<i>ydiJ</i>	putative FAD-linked oxidoreductase	1590	1294
b1688	1769074	1770186	<i>ydiK</i>	UPF0118 family inner membrane protein	799	426
b1689	1770615	1770971	<i>ydiL</i>	putative HTH domain DNA-binding protein	153	155
b1690	1771071	1772285	<i>ydiM</i>	putative MFS transporter, membrane protein	27	266
b1691	1772512	1773777	<i>ydiN</i>	putative MFS transporter, membrane protein	15	169
b1692	1773789	1774655	<i>ydiB</i>	quinate/shikimate 5-dehydrogenase, NAD(P)-binding	36	60
b1693	1774686	1775444	<i>aroD</i>	3-dehydroquinase dehydratase	634	390
b1694	1775587	1777182	<i>ydiF</i>	putative acetyl-CoA:acetoacetyl-CoA transferase: alpha subunit/beta subunit	64	144
b1695	1777196	1778347	<i>ydiO</i>	putative acyl-CoA dehydrogenase	64	67
b1696	1779301	1778390	<i>ydiP</i>	putative DNA-binding transcriptional regulator	532	484
b1697	1779617	1780381	<i>ydiQ</i>	putative electron transfer flavoprotein subunit	15	67
b1698	1780401	1781339	<i>ydiR</i>	putative electron transfer flavoprotein, FAD-binding subunit	29	69
b1699	1781395	1782684	<i>ydiS</i>	putative oxidoreductase	36	113
b1700	1782681	1782974	<i>ydiT</i>	putative 3Fe-4S ferredoxin-type protein	5	17
b1701	1783031	1784677	<i>fadK</i>	short chain acyl-CoA synthetase, anaerobic	86	603
b1702	1787112	1784734	<i>ppsA</i>	phosphoenolpyruvate synthase	75522	18574
b1703	1787445	1788278	<i>ppsR</i>	PEP synthase kinase and PEP synthase pyrophosphorylase	3882	1665
b1704	1788435	1789481	<i>aroH</i>	3-deoxy-D-arabino-heptulosonate-7-phosphate synthase, tryptophan repressible	1315	1647
b1705	1789613	1789804	<i>ydiE</i>	hemin uptake protein HemP homolog	128	141
b1706	1791244	1789808	<i>ydiU</i>	UPF0061 family protein	1619	1510
b1707	1792020	1791307	<i>ydiV</i>	anti-FlhD4C2 factor, inactive EAL family phosphodiesterase	1415	1261
b1708	1792731	1792267	<i>nlpC</i>	putative C40 clan peptidase lipoprotein	1212	904
b1709	1793558	1792809	<i>btuD</i>	vitamin B12 ABC transporter ATPase	384	432
b1710	1794109	1793558	<i>btuE</i>	glutathione peroxidase	536	657
b1711	1795152	1794172	<i>btuC</i>	vitamin B12 ABC transporter permease	303	224
b1712	1795552	1795253	<i>ihfA</i>	integration host factor (IHF), DNA-binding protein, alpha subunit	10337	3792
b1713	1797944	1795557	<i>pheT</i>	phenylalanine tRNA synthetase, beta subunit	20431	5941
b1714	1798942	1797959	<i>pheS</i>	phenylalanine tRNA synthetase, alpha subunit	3282	754
b1716	1799749	1799393	<i>rplT</i>	50S ribosomal subunit protein L20	32578	15055
b1717	1799999	1799802	<i>rpmI</i>	50S ribosomal subunit protein L35	49633	48012
b1718	1800638	1800096	<i>infC</i>	translation initiation factor IF-3	53988	35203
b1719	1802570	1800642	<i>thrS</i>	threonyl-tRNA synthetase	54607	25575
b1722	1806083	1805325	<i>ydiY</i>	acid-inducible putative outer membrane protein	3054	424
b1723	1806370	1807299	<i>pfkB</i>	6-phosphofructokinase II	1311	441

b1724	1807400	1807690	<i>ydiZ</i>	uncharacterized protein	809	1897
b1725	1807796	1808656	<i>yniA</i>	fructosamine kinase family protein	15558	3307
b1726	1809233	1808697	<i>yniB</i>	putative inner membrane protein	1333	2604
b1727	1809380	1810048	<i>yniC</i>	2-deoxyglucose-6-P phosphatase	1352	622
b1728	1810211	1810801	<i>ydjM</i>	inner membrane protein regulated by LexA	186	199
b1729	1810934	1812325	<i>ydjN</i>	putative transporter	6503	2368
b1730	1813132	1812329	<i>ydjO</i>	uncharacterized protein	48	296
b1731	1813663	1813421	<i>cedA</i>	cell division modulator	43	97
b1732	1813867	1816128	<i>katE</i>	catalase HP11, heme d-containing	2816	5479
b1733	1817135	1816386	<i>chbG</i>	chito-oligosaccharide deacetylase	225	231
b1734	1818500	1817148	<i>chbF</i>	phospho-chitobiase; general 6-phospho-beta-glucosidase activity	402	312
b1735	1819447	1818605	<i>chbR</i>	repressor of chb operon for N,N'-diacetylchitobiose utilization	930	1223
b1736	1819805	1819455	<i>chbA</i>	N,N'-diacetylchitobiose-specific enzyme IIA component of PTS	587	237
b1737	1821214	1819856	<i>chbC</i>	N,N'-diacetylchitobiose-specific enzyme IIC component of PTS	1362	298
b1738	1821619	1821299	<i>chbB</i>	N,N'-diacetylchitobiose-specific enzyme IIB component of PTS	1778	371
b1739	1822256	1821918	<i>osmE</i>	osmotically-inducible lipoprotein	2780	4089
b1740	1822458	1823285	<i>nadE</i>	NAD synthetase, NH ₃ /glutamine-dependent	2364	2688
b1741	1823515	1824402	<i>cho</i>	endonuclease of nucleotide excision repair	298	1080
b1742	1824937	1824362	<i>ves</i>	cold- and stress-inducible protein	447	471
b1743	1825625	1825140	<i>spy</i>	periplasmic ATP-independent protein refolding chaperone, stress-induced	721	6312
b1744	1826923	1825955	<i>astE</i>	succinylglutamate desuccinylase	1166	433
b1745	1828259	1826916	<i>astB</i>	succinylarginine dihydrolase	1630	393
b1746	1829734	1828256	<i>astD</i>	succinylglutamic semialdehyde dehydrogenase	2355	438
b1747	1830765	1829731	<i>astA</i>	arginine succinyltransferase	4472	599
b1748	1831982	1830762	<i>astC</i>	succinylornithine transaminase, PLP-dependent	14756	1405
b1749	1832428	1833234	<i>xthA</i>	exonuclease III	2112	676
b1750	1833401	1834111	<i>ydjX</i>	TVP38/TMEM64 family inner membrane protein	942	1172
b1751	1834116	1834793	<i>ydjY</i>	putative ferredoxin-like lipoprotein	2269	262
b1752	1834808	1835515	<i>ydjZ</i>	TVP38/TMEM64 family inner membrane protein	489	147
b1753	1835515	1836063	<i>ynjA</i>	carboxymuconolactone decarboxylase family protein	224	80
b1754	1836073	1837239	<i>ynjB</i>	putative ABC transporter periplasmic binding protein	742	220
b1755	1837212	1838747	<i>ynjC</i>	putative ABC transporter permease	171	126
b1756	1838747	1839400	<i>ynjD</i>	putative ABC transporter ATPase	141	173
b1757	1839467	1840774	<i>ynjE</i>	molybdopterin synthase sulfurtransferase	5035	429
b1758	1841403	1840783	<i>ynjF</i>	CDP-alcohol phosphatidyltransferase family inner membrane protein	101	121
b1759	1841490	1841897	<i>nudG</i>	CTP pyrophosphohydrolase; also hydrolyzes 2-hydroxy-dATP, 8-hydroxy-dGTP, 5-hydroxy-CTP, dCTP and 5-methyl-dCTP	222	243
b1760	1842135	1841863	<i>ynjH</i>	DUF1496 family protein	327	251
b1761	1842371	1843714	<i>gdhA</i>	glutamate dehydrogenase, NADP-specific	1224	3870
b1762	1844871	1843831	<i>ynjI</i>	inner membrane protein	149	844
b1763	1846960	1844999	<i>topB</i>	DNA topoisomerase III	1819	851
b1764	1848008	1846965	<i>selD</i>	selenophosphate synthase	6080	1733
b1765	1848676	1848125	<i>ydjA</i>	putative oxidoreductase	1578	753
b1766	1848837	1850693	<i>sppA</i>	protease IV (signal peptide peptidase)	505	598
b1767	1850860	1851876	<i>ansA</i>	cytoplasmic L-asparaginase 1	1169	782
b1768	1851887	1852528	<i>pncA</i>	nicotinamidase/pyrazinamidase	1325	882
b1769	1853979	1852621	<i>ydjE</i>	putative MFS sugar transporter, membrane protein	226	568
b1770	1854854	1854096	<i>ydjF</i>	putative DNA-binding transcriptional regulator	2725	2284
b1771	1855971	1854991	<i>ydjG</i>	methylglyoxal reductase, NADH-dependent	142	162

b1772	1856928	1855981	<i>ydjH</i>	putative kinase	42	40
b1773	1857769	1856933	<i>ydjI</i>	putative aldolase	0	1
b1774	1858833	1857790	<i>ydjJ</i>	putative Zn-dependent NAD(P)-binding oxidoreductase	0	0
b1775	1860229	1858850	<i>ydjK</i>	putative MFS sugar transporter, membrane protein	48	277
b1776	1861332	1860256	<i>ydjL</i>	putative Zn-dependent NAD(P)-binding oxidoreductase	177	227
b1777	1861974	1861702	<i>yeaC</i>	DUF1315 family protein	10077	2972
b1778	1862429	1862016	<i>msrB</i>	methionine sulfoxide reductase B	7940	2777
b1779	1862771	1863766	<i>gapA</i>	glyceraldehyde-3-phosphate dehydrogenase A	269889	55820
b1780	1863850	1864734	<i>yeaD</i>	D-hexose-6-phosphate epimerase-like protein	8430	1484
b1781	1865636	1864782	<i>yeaE</i>	aldo-keto reductase, methylglyoxal to acetol, NADPH-dependent	963	775
b1782	1866472	1865726	<i>mipA</i>	scaffolding protein for murein synthesizing machinery	5170	2149
b1783	1866908	1868842	<i>yeaG</i>	protein kinase, endogenous substrate unidentified; autokinase	17752	12593
b1784	1868955	1870238	<i>yeaH</i>	UPF0229 family protein	3203	3578
b1785	1870385	1871860	<i>yeaI</i>	putative membrane-anchored diguanylate cyclase	99	908
b1786	1872041	1873531	<i>yeaJ</i>	putative diguanylate cyclase	337	1228
b1787	1873574	1874077	<i>yeaK</i>	aminoacyl-tRNA editing domain protein	561	411
b1788	1874182	1874078	<i>yoaI</i>	uncharacterized protein	0	2
b1789	1874352	1874798	<i>yeaL</i>	UPF0756 family putative inner membrane protein	83	97
b1790	1875576	1874755	<i>yeaM</i>	putative DNA-binding transcriptional regulator	164	415
b1791	1875673	1876854	<i>yeaN</i>	putative MFS transporter, inner membrane protein	166	339
b1792	1876909	1877256	<i>yeaO</i>	DUF488 family protein	994	566
b1793	1877532	1877278	<i>yoaF</i>	DUF333 family outer membrane lipoprotein	343	259
b1794	1877715	1878740	<i>yeaP</i>	diguanylate cyclase	1094	1964
b1795	1879255	1879007	<i>yeaQ</i>	UPF0410 family protein	1071	1212
b1796	1879585	1879403	<i>yoaG</i>	uncharacterized protein	10	21
b1797	1879948	1879589	<i>yeaR</i>	DUF1971 family protein, nitrate-inducible	25	80
b1798	1880759	1880121	<i>leuE</i>	leucine efflux protein	443	550
b1799	1881809	1880886	<i>dmlR</i>	transcriptional activator of dmlA	1597	556
b1800	1881912	1882997	<i>dmlA</i>	D-malate oxidase, NAD-dependent; putative tartrate dehydrogenase	276	285
b1801	1883188	1884633	<i>yeaV</i>	putative transporter	90	557
b1802	1884665	1885789	<i>yeaW</i>	putative YeaWX dioxygenase alpha subunit; 2Fe-2S cluster	78	183
b1803	1885845	1886810	<i>yeaX</i>	putative YeaWX dioxygenase beta subunit, reductase component	82	513
b1804	1887991	1886864	<i>rnd</i>	ribonuclease D	1823	919
b1805	1889746	1888061	<i>fadD</i>	acyl-CoA synthetase (long-chain-fatty-acid--CoA ligase)	24024	7588
b1806	1890532	1889951	<i>yeaY</i>	Slp family lipoprotein, RpoE-regulated	908	3129
b1807	1891267	1890572	<i>tsaB</i>	tRNA(ANN) t(6)A37 threonylcarbamoyladenine modification protein; binding partner and protease for TsaD	695	349
b1808	1893235	1891325	<i>yoaA</i>	putative ATP-dependent helicase, DinG family	570	749
b1809	1893367	1893711	<i>yoaB</i>	putative reactive intermediate deaminase	2960	1846
b1810	1894133	1894432	<i>yoaC</i>	DUF1889 family protein	2645	4410
b1811	1894731	1894552	<i>yoaH</i>	UPF0181 family protein	275	446
b1812	1894805	1896166	<i>pabB</i>	aminodeoxychorismate synthase, subunit I	579	607
b1813	1896170	1896748	<i>nudL</i>	putative CoA pyrophosphohydrolase, weak 3-phosphohydroxypyruvate phosphatase	182	235
b1814	1896932	1898296	<i>sdaA</i>	L-serine dehydratase 1	11779	3709
b1815	1898427	1900025	<i>yoaD</i>	putative membrane-anchored cyclic-di-GMP phosphodiesterase, regulator of cellulose production	176	551
b1816	1901585	1900029	<i>yoaE</i>	putative membrane protein/conserved protein	981	1229
b1817	1902048	1903019	<i>manX</i>	fused mannose-specific PTS enzymes: IIA component/IIB component	131011	6293
b1818	1903082	1903882	<i>manY</i>	mannose-specific enzyme IIC component of PTS	56768	3040

b1819	1903895	1904746	<i>manZ</i>	mannose-specific enzyme IID component of PTS	60234	4304
b1820	1904801	1905259	<i>yobD</i>	UPF0266 family inner membrane protein	71	92
b1821	1905688	1906254	<i>mntP</i>	putative Mn(2+) efflux pump, mntR-regulated	0	0
b1822	1907060	1906251	<i>rlmA</i>	23S rRNA m(1)G745 methyltransferase, SAM-dependent	0	0
b1825	1908548	1908261	<i>yebO</i>	putative inner membrane protein	513	1673
b1826	1908766	1908623	<i>mgrB</i>	regulatory peptide for PhoPQ, feedback inhibition	81	621
b1827	1910099	1909308	<i>kdgR</i>	KDG regulon transcriptional repressor	2900	1965
b1828	1910276	1911649	<i>yebQ</i>	putative transporter	201	443
b1829	1912576	1911695	<i>htpX</i>	putative endopeptidase	3792	7982
b1830	1914816	1912768	<i>prc</i>	carboxy-terminal protease for penicillin-binding protein 3	6328	4118
b1831	1915534	1914836	<i>proQ</i>	RNA chaperone, putative ProP translation regulator	9531	3293
b1832	1916128	1915631	<i>msrC</i>	free methionine-(R)-sulfoxide reductase	1302	1321
b1833	1916258	1917541	<i>yebS</i>	inner membrane PqiA domain protein	474	1488
b1834	1917510	1920143	<i>yebT</i>	MCE domain protein	1338	1144
b1835	1920223	1921662	<i>rsmF</i>	16S rRNA m(5)C1407 methyltransferase, SAM-dependent	401	631
b1836	1921780	1922016	<i>yebV</i>	uncharacterized protein	2658	16568
b1837	1922121	1922312	<i>yebW</i>	uncharacterized protein	129	448
b1838	1922969	1922313	<i>pphA</i>	serine/threonine-specific protein phosphatase 1	137	793
b1839	1923706	1923365	<i>yebY</i>	DUF2511 family protein	1852	2812
b1840	1924591	1923719	<i>yebZ</i>	inner membrane protein	730	1007
b1841	1924969	1924595	<i>yobA</i>	CopC family protein	1219	3483
b1842	1925108	1925338	<i>holE</i>	DNA polymerase III, theta subunit	169	845
b1843	1925440	1926096	<i>yobB</i>	C-N hydrolase family protein	417	900
b1844	1926120	1926782	<i>exoX</i>	exodeoxyribonuclease 10; DNA exonuclease X	364	696
b1845	1928839	1926779	<i>ptrB</i>	protease II	1024	1487
b1846	1929707	1929048	<i>yebE</i>	DUF533 family inner membrane protein	1981	6659
b1847	1930390	1930034	<i>yebF</i>	extracellular Colicin M immunity family protein	2271	1655
b1848	1930747	1930457	<i>yebG</i>	DNA damage-inducible protein regulated by LexA	1860	8826
b1849	1930881	1932059	<i>purT</i>	phosphoribosylglycinamide formyltransferase 2	338	1015
b1850	1932756	1932115	<i>eda</i>	KHG/KDPG aldolase; 2-dehydro-3-deoxy-phosphogluconate/4-hydroxy-2-oxoglutarate aldolase	2628	257
b1851	1934604	1932793	<i>edd</i>	6-phosphogluconate dehydratase	2329	399
b1852	1936314	1934839	<i>zwf</i>	glucose-6-phosphate 1-dehydrogenase	5166	1751
b1853	1936652	1937521	<i>yebK</i>	putative DNA-binding transcriptional regulator	1231	1180
b1854	1937649	1939091	<i>pykA</i>	pyruvate kinase II	14796	4950
b1855	1940193	1939222	<i>lpxM</i>	myristoyl-acyl carrier protein (ACP)-dependent acyltransferase	703	1071
b1856	1941635	1940313	<i>mepM</i>	murein DD-endopeptidase, space-maker hydrolase, septation protein	1490	2353
b1857	1942583	1941651	<i>znuA</i>	zinc ABC transporter periplasmic binding protein	2131	1463
b1858	1942662	1943417	<i>znuC</i>	zinc ABC transporter ATPase	1121	1011
b1859	1943414	1944199	<i>znuB</i>	zinc ABC transporter permease	292	500
b1860	1945356	1944346	<i>ruvB</i>	ATP-dependent DNA helicase, component of RuvABC resolvasome	605	548
b1861	1945976	1945365	<i>ruvA</i>	component of RuvABC resolvasome, regulatory subunit	1274	1612
b1862	1946251	1946853	<i>yebB</i>	DUF830 family protein	48	250
b1863	1947376	1946855	<i>ruvC</i>	component of RuvABC resolvasome, endonuclease	1075	290
b1864	1948151	1947411	<i>yebC</i>	UPF0082 family protein	4185	1273
b1865	1948632	1948180	<i>nudB</i>	dihydroneopterin triphosphate pyrophosphatase	1037	425
b1866	1950522	1948750	<i>aspS</i>	aspartyl-tRNA synthetase	8406	1899
b1867	1950832	1951398	<i>yecD</i>	isochorismatase family protein	306	245
b1868	1951395	1952213	<i>yecE</i>	UPF0759 family protein	135	220
b1869	1952266	1952661	<i>yecN</i>	MAPEG family inner membrane protein	289	181
b1870	1952702	1953445	<i>cmoA</i>	carboxy-SAM synthase	717	311

b1871	1953442	1954413	<i>cmoB</i>	tRNA (cmo5U34)-carboxymethyltransferase, carboxy-SAM-dependent	716	363
b1872	1957007	1954578	<i>torZ</i>	trimethylamine N-oxide reductase system III, catalytic subunit	286	766
b1873	1958132	1957032	<i>torY</i>	TMAO reductase III (TorYZ), cytochrome c-type subunit	54	446
b1874	1959266	1958520	<i>cutC</i>	copper homeostasis protein	605	2716
b1875	1959846	1959280	<i>yecM</i>	putative metal-binding enzyme	277	273
b1876	1960062	1961795	<i>argS</i>	arginyl-tRNA synthetase	4021	2234
b1877	1961972	1962460	<i>yecT</i>	uncharacterized protein	49	471
b1878	1962972	1962580	<i>flhE</i>	proton seal during flagellar secretion	40	42
b1879	1965050	1962972	<i>flhA</i>	putative flagellar export pore protein	356	706
b1880	1966191	1965043	<i>flhB</i>	flagellin export apparatus, substrate specificity protein	112	589
b1881	1967037	1966393	<i>cheZ</i>	chemotaxis regulator, protein phosphatase for CheY	1890	461
b1882	1967437	1967048	<i>cheY</i>	chemotaxis regulator transmitting signal to flagellar motor component	2103	610
b1883	1968501	1967452	<i>cheB</i>	fused chemotaxis regulator: protein-glutamate methylesterase in two-component regulatory system with CheA	869	375
b1884	1969364	1968504	<i>cheR</i>	chemotaxis regulator, protein-glutamate methyltransferase	754	487
b1885	1970984	1969383	<i>tap</i>	methyl-accepting protein IV	3096	2191
b1886	1972691	1971030	<i>tar</i>	methyl-accepting chemotaxis protein II	5474	6199
b1887	1973339	1972836	<i>cheW</i>	purine-binding chemotaxis protein	2393	1390
b1888	1975324	1973360	<i>cheA</i>	fused chemotactic sensory histidine kinase in two-component regulatory system with CheB and CheY: sensory histidine kinase/signal sensing protein	6919	3815
b1889	1976255	1975329	<i>motB</i>	protein that enables flagellar motor rotation	1362	1659
b1890	1977139	1976252	<i>motA</i>	proton conductor component of flagella motor	1717	1726
b1891	1977844	1977266	<i>flhC</i>	flagellar class II regulon transcriptional activator, with FlhD	630	1028
b1892	1978197	1977847	<i>flhD</i>	flagellar class II regulon transcriptional activator, with FlhC	232	438
b1893	1979021	1978518	<i>insB1</i>	IS1 transposase B	721	1067
b1894	1979215	1978940	<i>insA</i>	IS1 repressor TnpA	96	513
b1895	1979753	1980181	<i>uspC</i>	universal stress protein	848	742
b1896	1981612	1980188	<i>otsA</i>	trehalose-6-phosphate synthase	2019	6728
b1897	1982387	1981587	<i>otsB</i>	trehalose-6-phosphate phosphatase, biosynthetic	892	4522
b1900	1985069	1983555	<i>araG</i>	L-arabinose ABC transporter ATPase	872	813
b1901	1986128	1985139	<i>araF</i>	L-arabinose ABC transporter periplasmic binding protein	1530	631
b1902	1986925	1987428	<i>ftnB</i>	ferritin B, putative ferrous iron reservoir	9584	2602
b1904	1988222	1988545	<i>yecR</i>	lipoprotein, function unknown	58	586
b1905	1988716	1989213	<i>ftnA</i>	ferritin iron storage protein (cytoplasmic)	4824	12481
b1906	1989490	1989251	<i>yecH</i>	DUF2492 family protein	374	593
b1907	1989681	1990892	<i>tyrP</i>	tyrosine transporter	143	372
b1908	1991619	1990954	<i>yecA</i>	UPF0149 family protein	3550	3296
b1912	1992817	1992269	<i>pgsA</i>	phosphatidylglycerophosphate synthetase	1435	580
b1913	1994706	1992874	<i>uvrC</i>	excinuclease UvrABC, endonuclease subunit	2458	1726
b1914	1995359	1994703	<i>uvrY</i>	response regulator in two-component regulatory system with BarA	2826	2315
b1915	1995818	1996042	<i>yecF</i>	DUF2594 family protein	830	507
b1916	1996832	1996110	<i>sdiA</i>	quorum-sensing transcriptional activator	953	882
b1917	1997814	1997062	<i>yecC</i>	putative ABC transporter ATPase	549	259
b1918	1998479	1997811	<i>yecS</i>	ABC family putative inner membrane permease	308	145
b1919	1999480	1998494	<i>dcyD</i>	D-cysteine desulphydrase, PLP-dependent	1753	864
b1920	2000385	1999585	<i>fliY</i>	cystine transporter subunit	24967	8253
b1921	2001024	2000473	<i>fliZ</i>	RpoS antagonist; putative regulator of FlhA activity	1485	5956
b1922	2001789	2001070	<i>fliA</i>	RNA polymerase, sigma 28 (sigma F) factor	1759	6220

b1923	2003606	2002110	<i>fliC</i>	flagellar filament structural protein (flagellin)	157229	50994
b1924	2003872	2005278	<i>fliD</i>	flagellar filament capping protein	4370	4099
b1925	2005303	2005713	<i>fliS</i>	flagellar protein potentiates polymerization	1192	803
b1926	2005713	2006078	<i>fliT</i>	putative flagellar synthesis and assembly chaperone	429	475
b1927	2006156	2007643	<i>amyA</i>	cytoplasmic alpha-amylase	5052	3291
b1928	2008090	2007677	<i>yedD</i>	lipoprotein	1248	591
b1929	2008277	2009482	<i>yedE</i>	UPF0394 family sulphur transport domain-containing inner membrane protein	4743	386
b1930	2009479	2009712	<i>yedF</i>	putative TusA family sulfurtransferase	2107	186
b1931	2009821	2010489	<i>yedK</i>	DUF159 family protein	262	134
b1932	2010600	2011079	<i>yedL</i>	GNAT family putative N-acetyltransferase	90	182
b1937	2013014	2012700	<i>fliE</i>	flagellar basal-body component	36	166
b1938	2013229	2014887	<i>fliF</i>	flagellar basal-body MS-ring and collar protein	455	1607
b1939	2014880	2015875	<i>fliG</i>	flagellar motor switching and energizing component	457	911
b1940	2015868	2016554	<i>fliH</i>	negative regulator of FliI ATPase activity	206	459
b1941	2016554	2017927	<i>fliI</i>	flagellum-specific ATP synthase	253	439
b1942	2017946	2018389	<i>fliJ</i>	flagellar protein	142	369
b1943	2018386	2019513	<i>fliK</i>	flagellar hook-length control protein	794	1075
b1944	2019618	2020082	<i>fliL</i>	flagellar biosynthesis protein	398	1417
b1945	2020087	2021091	<i>fliM</i>	flagellar motor switching and energizing component	633	2324
b1946	2021088	2021501	<i>fliN</i>	flagellar motor switching and energizing component	330	385
b1947	2021504	2021869	<i>fliO</i>	flagellar biosynthesis protein	86	88
b1948	2021869	2022606	<i>fliP</i>	flagellar biosynthesis protein	155	280
b1949	2022616	2022885	<i>fliQ</i>	flagellar biosynthesis protein	55	156
b1950	2022893	2023678	<i>fliR</i>	flagellar export pore protein	338	530
b1951	2023968	2024591	<i>rcaA</i>	transcriptional regulator of colanic acid capsular biosynthesis	291	444
b1952	2024823	2024635	<i>dsrB</i>	uncharacterized protein	710	577
b1953	2024986	2025213	<i>yodD</i>	uncharacterized protein	842	1478
b1955	2025511	2026326	<i>yedP</i>	putative mannosyl-3-phosphoglycerate phosphatase	1241	1744
b1956	2028017	2026323	<i>yedQ</i>	putative membrane-anchored diguanylate cyclase	789	1727
b1957	2028370	2028188	<i>yodC</i>	uncharacterized protein	318	313
b1958	2029366	2028449	<i>yedI</i>	DUF808 family inner membrane protein	817	646
b1959	2029539	2030459	<i>yedA</i>	amino acid exporter for phenylalanine, threonine	298	198
b1960	2030918	2030448	<i>vsr</i>	DNA mismatch endonuclease of very short patch repair	27	197
b1961	2032317	2030899	<i>dcm</i>	DNA cytosine methyltransferase	28	227
b1962	2033079	2032384	<i>yedJ</i>	putative HD superfamily phosphohydrolase	168	396
b1963	2033484	2033119	<i>yedR</i>	inner membrane protein	21	215
b1967	2035835	2036686	<i>hchA</i>	glyoxalase III and Hsp31 molecular chaperone	1228	1780
b1968	2038152	2036794	<i>yedV</i>	putative sensory kinase in two-component regulatory system with YedW	236	1220
b1969	2038823	2038152	<i>yedW</i>	response regulator family protein	192	988
b1970	2038956	2039369	<i>hiuH</i>	hydroxyisourate hydrolase	94	272
b1971	2039478	2040482	<i>yedY</i>	membrane-anchored, periplasmic TMAO, DMSO reductase	357	1033
b1972	2040483	2041118	<i>yedZ</i>	inner membrane heme subunit for periplasmic YedYZ reductase	107	333
b1973	2041375	2042025	<i>zinT</i>	zinc and cadmium binding protein, periplasmic	420	552
b1974	2042368	2042898	<i>yodB</i>	cytochrome b561 homolog	1912	3267
b1976	2043651	2044448	<i>mtfA</i>	anti-repressor for DgsA(Mlc)	2829	2736
b1978	2044938	2052014	<i>yeeJ</i>	putative adhesin	795	2247
b1981	2053643	2054959	<i>shiA</i>	shikimate transporter	572	686
b1982	2055061	2056515	<i>amn</i>	AMP nucleosidase	3677	2474
b1983	2056858	2057574	<i>yeeN</i>	UPF0082 family protein	8314	4309
b1985	2059690	2058203	<i>yeeO</i>	putative multidrug exporter, MATE family	164	1342

b1987	2060914	2059964	<i>cbl</i>	ssuEADCB/tauABCD operon transcriptional activator	647	4647
b1988	2061933	2061016	<i>nac</i>	nitrogen assimilation regulon transcriptional regulator; autorepressor	101	427
b1990	2063323	2062391	<i>ldtA</i>	L,D-transpeptidase linking Lpp to murein	2096	1703
b1991	2064467	2063388	<i>cobT</i>	nicotinate-nucleotide--dimethylbenzimidazole phosphoribosyltransferase	574	494
b1992	2065222	2064479	<i>cobS</i>	cobalamin synthase	153	153
b1993	2065764	2065219	<i>cobU</i>	cobinamide kinase and cobinamide phosphate guanylyltransferase	327	314
b1994	2067321	2066305	<i>insH1</i>	IS5 transposase and trans-activator	618	847
b1996	2069857	2068952	<i>insD1</i>	IS2 transposase TnpB	652	819
b1997	2070180	2069815	<i>insC1</i>	IS2 repressor TnpA	403	429
b2000	2071539	2074658	<i>flu</i>	CP4-44 prophage; antigen 43 (Ag43) phase-variable biofilm formation autotransporter	4809	1064
b2001	2074779	2076311	<i>yeeR</i>	CP4-44 prophage; putative membrane protein	515	866
b2002	2076308	2076754	<i>yeeS</i>	CP4-44 prophage; putative DNA repair protein	33	31
b2003	2076817	2077038	<i>yeeT</i>	CP4-44 prophage; uncharacterized protein	6	19
b2004	2077112	2077480	<i>cbeA</i>	CP4-44 prophage; cytoskeleton bundling-enhancing factor A; CbtA antitoxin	19	37
b2005	2077569	2077943	<i>cbtA</i>	CP4-44 prophage; toxin of the YeeV-YeeU toxin-antitoxin system	106	127
b2007	2079361	2079032	<i>yeeX</i>	UPF0265 family protein	13086	11315
b2008	2080591	2079533	<i>yeeA</i>	putative transporter, FUSC family inner membrane protein	461	712
b2009	2081262	2080789	<i>sbmC</i>	DNA gyrase inhibitor	2011	4040
b2010	2082547	2081381	<i>dacD</i>	D-alanyl-D-alanine carboxypeptidase; penicillin-binding protein 6b	176	672
b2011	2082756	2084183	<i>sbcB</i>	exodeoxyribonuclease I; exonuclease I	1151	1704
b2012	2084453	2084226	<i>yeeD</i>	putative TusA family sulfurtransferase	1980	1001
b2013	2085525	2084467	<i>yeeE</i>	UPF0394 family inner membrane protein	6815	3376
b2014	2087062	2085704	<i>plaP</i>	putrescine importer, low affinity	5179	1614
b2015	2088258	2087329	<i>yeeY</i>	LysR family putative transcriptional regulator	779	1408
b2016	2089128	2088304	<i>yeeZ</i>	putative epimerase	3877	2688
b2017	2089713	2089462	<i>yefM</i>	antitoxin of the YoeB-YefM toxin-antitoxin system	1261	2621
b2019	2090192	2091091	<i>hisG</i>	ATP phosphoribosyltransferase	668	652
b2020	2091097	2092401	<i>hisD</i>	bifunctional histidinol dehydrogenase/ histidinol dehydrogenase	673	365
b2021	2092398	2093468	<i>hisC</i>	histidinol-phosphate aminotransferase	652	383
b2022	2093468	2094535	<i>hisB</i>	histidinol-phosphatase and imidazoleglycerol-phosphate dehydratase	900	653
b2023	2094535	2095125	<i>hisH</i>	imidazole glycerol phosphate synthase, glutamine amidotransferase subunit	296	118
b2024	2095125	2095862	<i>hisA</i>	N-(5'-phospho-L-ribosyl-formimino)-5-amino-1- (5'-phosphoribosyl)-4-imidazolecarboxamide isomerase	408	180
b2025	2095844	2096620	<i>hisF</i>	imidazole glycerol phosphate synthase, catalytic subunit with HisH	499	269
b2026	2096614	2097225	<i>hisI</i>	phosphoribosyl-AMP cyclohydrolase and phosphoribosyl-ATP pyrophosphatase	1100	632
b2027	2098301	2097321	<i>wzzB</i>	regulator of length of O-antigen component of lipopolysaccharide chains	10319	15507
b2028	2099613	2098447	<i>ugd</i>	UDP-glucose 6-dehydrogenase	15394	32048
b2029	2101268	2099862	<i>gnd</i>	6-phosphogluconate dehydrogenase, decarboxylating	29965	4288
b2030	2102911	2101895	<i>insH1</i>	IS5 transposase and trans-activator	3143	2558
b2032	2104509	2103391	<i>wbbK</i>	lipopolysaccharide biosynthesis protein	243	786
b2033	2105084	2104494	<i>wbbJ</i>	putative lipopolysaccharide biosynthesis O-acetyl transferase	162	506
b2034	2106057	2105065	<i>wbbI</i>	d-Galf:alpha-d-Glc beta-1,6-galactofuranosyltransferase	304	773
b2035	2107226	2106060	<i>wbbH</i>	O-antigen polymerase	105	636
b2036	2108329	2107226	<i>glf</i>	UDP-galactopyranose mutase, FAD/NAD(P)-binding	500	3056
b2037	2109584	2108337	<i>wzxB</i>	putative polisoprenol-linked O-antigen transporter	130	1502

b2038	2110138	2109581	<i>rfbC</i>	dTDP-4-deoxyrhamnose-3,5-epimerase	135	420
b2039	2111019	2110138	<i>rfbA</i>	glucose-1-phosphate thymidyltransferase	429	857
b2040	2111976	2111077	<i>rfbD</i>	dTDP-L-rhamnose synthase, NAD(P)-dependent dTDP-4-dehydrorhamnose reductase subunit	195	920
b2041	2113061	2111976	<i>rfbB</i>	dTDP-glucose 4,6 dehydratase, NAD(P)-binding	188	512
b2042	2114327	2113434	<i>wcaN</i>	putative regulatory subunit for GalU	15408	4085
b2043	2115896	2114502	<i>wcaM</i>	colanic acid biosynthesis protein	156	305
b2044	2117127	2115907	<i>wcaL</i>	putative glycosyl transferase	60	144
b2045	2118404	2117124	<i>wcaK</i>	colanic acid biosynthesis protein	122	74
b2046	2120158	2118680	<i>wzcC</i>	putative colanic acid exporter	101	116
b2047	2121554	2120160	<i>wcaJ</i>	colanic biosynthesis UDP-glucose lipid carrier transferase	100	67
b2048	2122979	2121609	<i>cpsG</i>	phosphomannomutase	230	70
b2049	2124520	2123084	<i>cpsB</i>	mannose-1-phosphate guanyltrtransferase	213	108
b2050	2125746	2124523	<i>wcaI</i>	putative glycosyl transferase	155	46
b2051	2126222	2125743	<i>wcaH</i>	GDP-mannose mannosyl hydrolase	62	34
b2052	2127190	2126225	<i>wcaG</i>	bifunctional GDP-fucose synthetase: GDP-4-dehydro-6-deoxy-D-mannose epimerase/ GDP-4-dehydro-6-L-deoxygalactose reductase	240	40
b2053	2128314	2127193	<i>gmd</i>	GDP-D-mannose dehydratase, NAD(P)-binding	512	115
b2054	2128888	2128340	<i>wcaF</i>	putative acyl transferase	53	41
b2055	2129650	2128904	<i>wcaE</i>	putative glycosyl transferase	108	39
b2056	2130878	2129661	<i>wcaD</i>	putative colanic acid polymerase	108	272
b2057	2132070	2130853	<i>wcaC</i>	putative glycosyl transferase	63	59
b2058	2132555	2132067	<i>wcaB</i>	putative acyl transferase	33	44
b2059	2133397	2132558	<i>wcaA</i>	putative glycosyl transferase	106	177
b2060	2135652	2133490	<i>wzc</i>	colanic acid production tyrosine-protein kinase; autokinase; Ugd phosphorylase	209	165
b2061	2136098	2135655	<i>wzb</i>	colanic acid production protein-tyrosine-phosphatase; Wzc-P dephosphorylase	32	14
b2062	2137243	2136104	<i>wza</i>	colanic acid export protein; outer membrane auxillary lipoprotein	123	77
b2063	2137902	2139485	<i>yegH</i>	inner membrane protein	788	756
b2064	2141612	2139759	<i>asmA</i>	suppressor of OmpF assembly mutants; putative outer membrane protein assembly factor; inner membrane-anchored periplasmic protein	2639	2507
b2065	2142215	2141634	<i>dcd</i>	deoxycytidine triphosphate deaminase; dCTP deaminase	2080	572
b2066	2142948	2142307	<i>udk</i>	uridine/cytidine kinase	691	380
b2067	2143266	2146583	<i>yegE</i>	putative diguanylate cyclase	1794	2014
b2068	2147540	2146692	<i>alkA</i>	3-methyl-adenine DNA glycosylase II	156	223
b2069	2147674	2149026	<i>yegD</i>	Hsp70 chaperone family protein	141	219
b2070	2150985	2149039	<i>yegI</i>	protein kinase-related putative non-specific DNA-binding protein	281	499
b2071	2151185	2151646	<i>yegJ</i>	uncharacterized protein	82	222
b2072	2152472	2151711	<i>yegK</i>	ser/thr phosphatase-related protein	16	59
b2073	2153128	2152469	<i>yegL</i>	VMA domain protein	39	153
b2074	2154016	2155263	<i>mdtA</i>	multidrug efflux system, subunit A	360	681
b2075	2155263	2158385	<i>mdtB</i>	multidrug efflux system, subunit B	428	386
b2076	2158386	2161463	<i>mdtC</i>	multidrug efflux system, subunit C	282	356
b2077	2161464	2162879	<i>iceT</i>	putative citrate/iron-citrate/zinc-citrate efflux transporter	85	198
b2078	2162876	2164279	<i>baeS</i>	sensory histidine kinase in two-component regulatory system with BaeR	137	188
b2079	2164276	2164998	<i>baeR</i>	response regulator in two-component regulatory system with BaeS	402	515
b2080	2165189	2165521	<i>yegP</i>	UPF0339 family protein	767	1354
b2081	2165668	2167029	<i>yegQ</i>	putative peptidase	1047	895
b2082	2167520	2167302	<i>ogrK</i>	orphan Ogr protein, positive regulator of P2 growth	226	267
b2085	2168306	2167989	<i>yegR</i>	uncharacterized protein	12	307

b2086	2168712	2169611	<i>yegS</i>	phosphatidylglycerol kinase, metal-dependent	2239	1249
b2088	2170236	2170535	<i>insE1</i>	IS3 transposase A	106	309
b2089	2170532	2171398	<i>insF1</i>	IS3 transposase B	106	239
b2091	2172873	2171833	<i>gatD</i>	galactitol-1-phosphate dehydrogenase, Zn-dependent and NAD(P)-binding	35	142
b2093	2174566	2174282	<i>gatB</i>	galactitol-specific enzyme IIB component of PTS	5	120
b2094	2175049	2174597	<i>gatA</i>	galactitol-specific enzyme IIA component of PTS	7	33
b2095	2176321	2175059	<i>gatZ</i>	D-tagatose 1,6-bisphosphate aldolase 2, subunit	67	259
b2096	2177204	2176350	<i>gatY</i>	D-tagatose 1,6-bisphosphate aldolase 2, catalytic subunit	4399	11404
b2097	2178564	2177512	<i>fbaB</i>	fructose-bisphosphate aldolase class I	2020	2328
b2098	2178821	2180098	<i>yegT</i>	nucleoside transporter, low affinity	179	518
b2099	2180095	2181099	<i>yegU</i>	ADP-ribosylglycohydrolase family protein	188	99
b2100	2181096	2182061	<i>yegV</i>	putative kinase	169	106
b2101	2182781	2182035	<i>yegW</i>	putative DNA-binding transcriptional regulator	446	220
b2102	2183651	2182833	<i>yegX</i>	putative family 25 glycosyl hydrolase	203	747
b2103	2184516	2183716	<i>thiD</i>	hydroxy-methylpyrimidine kinase and hydroxy-phosphomethylpyrimidine kinase	106	202
b2104	2185301	2184513	<i>thiM</i>	hydroxyethylthiazole kinase	88	160
b2105	2185796	2185524	<i>rcnR</i>	transcriptional repressor of rcnA	46	323
b2106	2185917	2186741	<i>rcnA</i>	membrane protein conferring nickel and cobalt resistance	125	342
b2107	2186960	2187298	<i>rcnB</i>	periplasmic modulator of Ni and Co efflux	738	1055
b2108	2188414	2187380	<i>yehA</i>	putative fimbrial-like adhesin protein	49	492
b2109	2190910	2188430	<i>yehB</i>	putative outer membrane protein	122	788
b2110	2191645	2190926	<i>yehC</i>	putative periplasmic pilin chaperone	88	175
b2111	2192222	2191680	<i>yehD</i>	putative fimbrial-like adhesin protein	1468	527
b2112	2192796	2192515	<i>yehE</i>	DUF2574 family protein	311	829
b2113	2194168	2193059	<i>mrp</i>	antiporter inner membrane protein	5238	1980
b2114	2194300	2196333	<i>metG</i>	methionyl-tRNA synthetase	4286	1594
b2118	2200279	2203911	<i>yehI</i>	DUF4132 domain-containing protein	182	888
b2119	2204596	2205684	<i>yehL</i>	putative hexameric AAA+ MoxR family ATPase	16	38
b2120	2205695	2207974	<i>yehM</i>	uncharacterized protein	47	145
b2121	2207967	2209103	<i>yehP</i>	VMA domain putative YehL ATPase stimulator	22	109
b2123	2211225	2211686	<i>yehR</i>	lipoprotein, DUF1307 family	115	427
b2124	2212196	2211726	<i>yehS</i>	DUF1456 family protein	919	1602
b2125	2212962	2212243	<i>yehT</i>	putative response regulator in two-component system with YehU	795	511
b2126	2214644	2212959	<i>yehU</i>	inner membrane putative sensory kinase in two-component system with YehT	1478	1772
b2127	2214866	2215597	<i>mlrA</i>	transcriptional activator of csgD and csgBA	602	714
b2128	2216476	2215745	<i>yehW</i>	putative ABC transporter permease	123	198
b2129	2217407	2216481	<i>yehX</i>	putative ABC transporter ATPase	120	121
b2130	2218557	2217400	<i>yehY</i>	putative ABC transporter permease	112	117
b2131	2219481	2218564	<i>osmF</i>	putative ABC transporter periplasmic binding protein	762	811
b2132	2221989	2219692	<i>bglX</i>	beta-D-glucoside glucosylhydrolase, periplasmic	3201	1116
b2133	2222185	2223900	<i>dld</i>	D-lactate dehydrogenase, FAD-binding, NADH independent	10051	3305
b2134	2224870	2223938	<i>pbpG</i>	D-alanyl-D-alanine endopeptidase	573	423
b2135	2225631	2225044	<i>yohC</i>	Yip1 family inner membrane protein	528	1166
b2136	2225801	2226379	<i>yohD</i>	DedA family inner membrane protein	406	411
b2137	2227270	2226509	<i>yohF</i>	putative oxidoreductase	281	609
b2140	2230385	2229438	<i>dusC</i>	tRNA-dihydrouridine synthase C	89	203
b2141	2230624	2231022	<i>yohJ</i>	UPF0299 family inner membrane protein	95	142
b2142	2231019	2231714	<i>yohK</i>	LrgB family inner membrane protein	200	155
b2143	2231844	2232728	<i>cdd</i>	cytidine/deoxycytidine deaminase	4027	223
b2144	2232878	2233597	<i>sanA</i>	DUF218 superfamily vancomycin high temperature	147	309

				exclusion protein		
b2145	2233600	2233839	<i>yeiS</i>	DUF2542 family protein	153	156
b2146	2234033	2235271	<i>preT</i>	dihydropyrimidine dehydrogenase, NADH-dependent, subunit N	2758	284
b2147	2235265	2236500	<i>preA</i>	dihydropyrimidine dehydrogenase, NADH-dependent, subunit C	1519	334
b2148	2237753	2236743	<i>mglC</i>	methyl-galactoside transporter subunit	5460	580
b2149	2239289	2237769	<i>mglA</i>	methyl-galactoside ABC transporter ATPase	13988	1159
b2150	2240348	2239350	<i>mglB</i>	methyl-galactoside transporter subunit	64595	2503
b2151	2241668	2240628	<i>galS</i>	galactose- and fucose-inducible galactose regulon transcriptional isorepressor; mgl operon transcriptional repressor; autorepressor	9928	157
b2152	2242967	2241810	<i>yeiB</i>	DUF418 family putative inner membrane protein	350	222
b2153	2243652	2242984	<i>folE</i>	GTP cyclohydrolase I	4708	1672
b2154	2243910	2244746	<i>yeiG</i>	S-formylglutathione hydrolase	2938	2220
b2155	2246769	2244778	<i>cirA</i>	colicin IA outer membrane receptor and translocator; ferric iron-catecholate transporter	5420	693
b2156	2248532	2247063	<i>lysP</i>	lysine transporter	868	731
b2157	2249618	2248737	<i>yeiE</i>	putative DNA-binding transcriptional regulator	1185	531
b2158	2249717	2250766	<i>yeiH</i>	UPF0324 family inner membrane protein	229	233
b2159	2250840	2251697	<i>nfo</i>	endonuclease IV with intrinsic 3'-5' exonuclease activity	974	606
b2160	2251700	2252788	<i>yeiI</i>	putative kinase	388	312
b2161	2254145	2252895	<i>nupX</i>	nucleoside permease	54	312
b2162	2255186	2254245	<i>rihB</i>	ribonucleoside hydrolase 2	72	73
b2163	2255355	2256014	<i>yeiL</i>	putative transcriptional regulator	141	169
b2164	2257335	2256085	<i>psuT</i>	putative nucleoside transporter	198	414
b2165	2258367	2257429	<i>psuG</i>	pseudouridine 5'-phosphate glycosidase	389	911
b2166	2259296	2258355	<i>psuK</i>	pseudouridine kinase	287	851
b2167	2261410	2259719	<i>fruA</i>	fused fructose-specific PTS enzymes: IIBcomponent/IIC components	11076	1387
b2168	2262365	2261427	<i>fruK</i>	fructose-1-phosphate kinase	6754	587
b2169	2263495	2262365	<i>fruB</i>	fused fructose-specific PTS enzymes: IIA component/HPr component	8708	1198
b2170	2263863	2265044	<i>setB</i>	lactose/glucose efflux system	93	211
b2171	2265450	2266022	<i>yeiP</i>	elongation factor P-like protein	3775	1258
b2172	2266245	2267711	<i>yeiQ</i>	putative NAD-dependent D-mannonate oxidoreductase	12349	574
b2173	2267829	2268815	<i>yeiR</i>	Zn-stimulated GTPase involved in zinc homeostasis; mutants are cadmium and EDTA sensitive; Zn(2+) binding protein	216	89
b2174	2268854	2269567	<i>lpxT</i>	lipid A 1-diphosphate synthase; undecaprenyl pyrophosphate:lipid A 1-phosphate phosphotransferase	238	278
b2175	2269979	2270545	<i>mepS</i>	murein DD-endopeptidase, space-maker hydrolase, mutational suppressor of prc thermosensitivity, outer membrane lipoprotein, weak murein LD-carboxypeptidase	5375	4588
b2176	2270726	2272282	<i>rtn</i>	resistance protein for phages lambda and N4, putative membrane-anchored cyclic-di-GMP phosphodiesterase	255	521
b2177	2272364	2274178	<i>yejA</i>	microcin C ABC transporter periplasmic binding protein	1221	1471
b2178	2274179	2275273	<i>yejB</i>	microcin C ABC transporter permease	203	302
b2179	2275273	2276298	<i>yejE</i>	microcin C ABC transporter permease	245	493
b2180	2276300	2277889	<i>yejF</i>	microcin C ABC transporter ATPase	826	3439
b2181	2278237	2277893	<i>yejG</i>	uncharacterized protein	3289	2856
b2182	2279760	2278570	<i>bcr</i>	bicyclomycin/cysteine/sulfonamide efflux transporter	558	1011
b2183	2280483	2279788	<i>rsuA</i>	16S rRNA pseudouridine(516) synthase	900	818
b2184	2280632	2282392	<i>yejH</i>	putative ATP-dependent DNA or RNA helicase	304	357
b2185	2282517	2282801	<i>rplY</i>	50S ribosomal subunit protein L25	8999	2867
b2186	2283947	2282940	<i>yejK</i>	spermidine nucleoid-associated protein	3345	1355
b2187	2284129	2284356	<i>yejL</i>	UPF0352 family protein	465	436

b2188	2284376	2286136	<i>yejM</i>	essential inner membrane DUF3413 domain-containing protein; lipid A production and membrane permeability factor	1428	2472
b2192	2290081	2289065	<i>insH1</i>	IS5 transposase and trans-activator	3143	2558
b2193	2290500	2291147	<i>narP</i>	response regulator in two-component regulatory system with NarQ	960	563
b2194	2292410	2291358	<i>ccmH</i>	heme lyase, CcmH subunit	385	265
b2195	2292964	2292407	<i>dsbE</i>	periplasmic thioredoxin of cytochrome c-type biogenesis	179	87
b2196	2294904	2292961	<i>ccmF</i>	heme lyase, CcmF subunit	358	240
b2197	2295380	2294901	<i>ccmE</i>	periplasmic heme chaperone	160	176
b2198	2295586	2295377	<i>ccmD</i>	cytochrome c biogenesis protein; heme export ABC transporter holo-CcmE release factor	25	15
b2199	2296320	2295583	<i>ccmC</i>	heme export ABC transporter permease; CcmE-interacting protein	353	118
b2200	2297024	2296362	<i>ccmB</i>	heme export ABC transporter permease	133	66
b2201	2297644	2297021	<i>ccmA</i>	heme export ABC transporter ATPase	794	490
b2202	2298259	2297657	<i>napC</i>	quinol dehydrogenase, electron source for NapAB	1176	512
b2203	2298718	2298269	<i>napB</i>	nitrate reductase, small, cytochrome C550 subunit, periplasmic	489	175
b2204	2299578	2298715	<i>napH</i>	ferredoxin-type protein	230	197
b2205	2300260	2299565	<i>napG</i>	ferredoxin-type protein	311	129
b2206	2302753	2300267	<i>napA</i>	nitrate reductase, periplasmic, large subunit	4362	1203
b2207	2303013	2302750	<i>napD</i>	assembly protein for periplasmic nitrate reductase	83	66
b2208	2303497	2303003	<i>napF</i>	ferredoxin-type protein, role in electron transfer to periplasmic nitrate reductase NapA	460	640
b2209	2303905	2304393	<i>eco</i>	ecotin, a serine protease inhibitor	3406	638
b2210	2306754	2305108	<i>mgo</i>	malate dehydrogenase, FAD/NAD(P)-binding domain	6715	1066
b2211	2308615	2306972	<i>yojI</i>	microcin J25 efflux ABC transporter permease/ATPase	1224	1469
b2212	2309341	2308691	<i>alkB</i>	oxidative demethylase of N1-methyladenine or N3-methylcytosine DNA lesions	129	85
b2213	2310405	2309341	<i>ada</i>	fused DNA-binding transcriptional dual regulator/O6-methylguanine-DNA methyltransferase	478	367
b2214	2311534	2310479	<i>apbE</i>	putative thiamine-synthetic flavin transferase lipoprotein	392	263
b2215	2312749	2311646	<i>ompC</i>	outer membrane porin protein C	86427	21992
b2216	2313488	2316160	<i>rscD</i>	phosphotransfer intermediate protein in two-component regulatory system with RcsBC	4319	9232
b2217	2316177	2316827	<i>rscB</i>	response regulator in two-component regulatory system with RcsC and YojN	8828	7273
b2218	2319876	2317027	<i>rscC</i>	hybrid sensory kinase in two-component regulatory system with RcsB and YojN	2321	2240
b2219	2320043	2321869	<i>atoS</i>	sensory histidine kinase in two-component regulatory system with AtoC	6040	2124
b2220	2321866	2323251	<i>atoC</i>	fused response regulator of ato operon, in two-component system with AtoS: response regulator/sigma54 interaction protein	3625	604
b2221	2323447	2324109	<i>atoD</i>	acetyl-CoA:acetoacetyl-CoA transferase, alpha subunit	14	58
b2222	2324109	2324759	<i>atoA</i>	acetyl-CoA:acetoacetyl-CoA transferase, beta subunit	9	46
b2223	2324756	2326078	<i>atoE</i>	short chain fatty acid transporter	31	111
b2224	2326109	2327293	<i>atoB</i>	acetyl-CoA acetyltransferase	41	122
b2225	2328143	2327367	<i>yfaP</i>	DUF2135 family protein, putative host defense protein	34	94
b2226	2329797	2328148	<i>yfaQ</i>	tandem DUF2300 domain protein, putative host defense protein	37	146
b2229	2334959	2334336	<i>yfaT</i>	DUF1175 family protein, putative host defense protein	19	44
b2230	2336644	2334956	<i>yfaA</i>	DUF2138 family protein, putative host defense protein	219	192
b2231	2339420	2336793	<i>gyrA</i>	DNA gyrase (type II topoisomerase), subunit A	16222	4514
b2232	2339567	2340289	<i>ubiG</i>	bifunctional 3-demethylubiquinone-9 3-methyltransferase/ 2-octaprenyl-6-hydroxy phenol methylase	372	497
b2233	2344169	2340417	<i>yfaL</i>	adhesin	333	1016
b2234	2344865	2347150	<i>nrdA</i>	ribonucleoside-diphosphate reductase 1, alpha subunit	6685	2049

b2235	2347384	2348514	<i>nrdB</i>	ribonucleoside-diphosphate reductase 1, beta subunit, ferritin-like protein	3990	842
b2236	2348514	2348768	<i>yfaE</i>	ferredoxin involved with ribonucleotide reductase diferric-tyrosyl radical (Y*) cofactor maintenance	518	181
b2237	2349472	2348822	<i>inaA</i>	acid-inducible Kdo/WaaP family putative kinase	994	1474
b2239	2351011	2349935	<i>glpQ</i>	periplasmic glycerophosphodiester phosphodiesterase	5396	11641
b2240	2352374	2351016	<i>glpT</i>	sn-glycerol-3-phosphate transporter	7529	5724
b2241	2352647	2354275	<i>glpA</i>	anaerobic sn-glycerol-3-phosphate dehydrogenase, large FAD/NAD(P)-binding subunit	864	1429
b2242	2354265	2355524	<i>glpB</i>	anaerobic sn-glycerol-3-phosphate dehydrogenase membrane anchor subunit	607	1381
b2243	2355521	2356711	<i>glpC</i>	anaerobic sn-glycerol-3-phosphate dehydrogenase, C subunit, 4Fe-4S iron-sulfur cluster	510	1204
b2244	2356904	2357803	<i>yfaD</i>	transposase_31 family protein	99	352
b2245	2358845	2358042	<i>rhmA</i>	2-keto-3-deoxy-L-rhamnonate aldolase	116	182
b2246	2360152	2358863	<i>rhmT</i>	putative L-rhamnonate transporter	51	107
b2247	2361414	2360209	<i>rhmD</i>	L-rhamnonate dehydratase	120	166
b2248	2362211	2361429	<i>rhmR</i>	putative DNA-binding transcriptional regulator for the rhm operon	82	149
b2249	2363633	2362431	<i>yfaY</i>	inactive PncC family protein	1131	535
b2250	2364275	2363733	<i>yfaZ</i>	outer membrane protein, putative porin	779	278
b2251	2364554	2364979	<i>nudI</i>	nucleoside triphosphatase	505	791
b2252	2365620	2365018	<i>ais</i>	putative LPS core heptose(II)-phosphate phosphatase	4307	10381
b2253	2365928	2367067	<i>arnB</i>	uridine 5'-(beta-1-threo-pentapyranosyl-4-ulose diphosphate) aminotransferase, PLP-dependent	11679	18102
b2254	2367071	2368039	<i>arnC</i>	undecaprenyl phosphate-L-Ara4FN transferase	10009	5433
b2255	2368039	2370021	<i>arnA</i>	fused UDP-L-Ara4N formyltransferase/UDP-GlcA C-4'-decarboxylase	27929	12747
b2256	2370018	2370908	<i>arnD</i>	undecaprenyl phosphate-alpha-L-ara4FN deformylase	5366	2996
b2257	2370908	2372560	<i>arnT</i>	4-amino-4-deoxy-L-arabinose transferase	3502	3284
b2258	2372892	2373278	<i>arnF</i>	undecaprenyl phosphate-alpha-L-ara4N exporter; flippase ArnEF subunit	395	1261
b2259	2373538	2373272	<i>pmrD</i>	inactive two-component system connector protein	861	1815
b2260	2375003	2373648	<i>menE</i>	O-succinylbenzoate-CoA ligase	392	228
b2261	2375962	2375000	<i>menC</i>	O-succinylbenzoyl-CoA synthase	920	266
b2262	2376819	2375962	<i>menB</i>	dihydroxynaphthoic acid synthetase	2259	272
b2263	2377592	2376834	<i>menH</i>	2-succinyl-6-hydroxy-2, 4-cyclohexadiene-1-carboxylate synthase	105	85
b2264	2379259	2377589	<i>menD</i>	2-succinyl-5-enolpyruvyl-6-hydroxy-3- cyclohexene-1-carboxylate synthase; SEPHCHC synthase	1303	439
b2265	2380643	2379348	<i>menF</i>	isochorismate synthase 2	782	703
b2266	2381027	2380722	<i>elaB</i>	putative membrane-anchored DUF883 family ribosome-binding protein	3692	3342
b2267	2381543	2381082	<i>elaA</i>	GNAT family putative N-acetyltransferase	1017	2067
b2268	2381608	2382525	<i>rbn</i>	RNase BN, tRNA processing enzyme	441	534
b2269	2382713	2383924	<i>elaD</i>	protease, capable of cleaving an AMC-ubiquitin model substrate	158	1048
b2270	2385722	2383995	<i>yfbK</i>	Von Willebrand factor domain putative lipoprotein	213	917
b2271	2385860	2386831	<i>yfbL</i>	putative M28A family peptidase	13	308
b2272	2386934	2387437	<i>yfbM</i>	DUF1877 family protein	158	495
b2273	2388426	2387710	<i>yfbN</i>	uncharacterized protein	17	250
b2274	2388635	2389057	<i>yfbO</i>	uncharacterized protein	34	331
b2275	2389116	2389964	<i>yfbP</i>	TPR-like repeats-containing protein	95	273
b2276	2391505	2390048	<i>nuoN</i>	NADH:ubiquinone oxidoreductase, membrane subunit N	6355	642
b2277	2393041	2391512	<i>nuoM</i>	NADH:ubiquinone oxidoreductase, membrane subunit M	5884	689
b2278	2395046	2393205	<i>nuoL</i>	NADH:ubiquinone oxidoreductase, membrane subunit L	6275	927
b2279	2395345	2395043	<i>nuoK</i>	NADH:ubiquinone oxidoreductase, membrane subunit K	668	92
b2280	2395896	2395342	<i>nuoJ</i>	NADH:ubiquinone oxidoreductase, membrane subunit J	3121	826
b2281	2396450	2395908	<i>nuoI</i>	NADH:ubiquinone oxidoreductase, chain I	3357	647

b2282	2397442	2396465	<i>nuoH</i>	NADH:ubiquinone oxidoreductase, membrane subunit H	4969	571
b2283	2400165	2397439	<i>nuoG</i>	NADH:ubiquinone oxidoreductase, chain G	17221	2828
b2284	2401555	2400218	<i>nuoF</i>	NADH:ubiquinone oxidoreductase, chain F	9757	1136
b2285	2402052	2401552	<i>nuoE</i>	NADH:ubiquinone oxidoreductase, chain E	5743	1689
b2286	2403845	2402055	<i>nuoC</i>	NADH:ubiquinone oxidoreductase, fused CD subunit	18340	2947
b2287	2404613	2403951	<i>nuoB</i>	NADH:ubiquinone oxidoreductase, chain B	12234	1722
b2288	2405072	2404629	<i>nuoA</i>	NADH:ubiquinone oxidoreductase, membrane subunit A	5249	1181
b2289	2406641	2405703	<i>lrhA</i>	transcriptional repressor of flagellar, motility and chemotaxis genes	3030	3561
b2290	2407561	2408778	<i>alaA</i>	glutamate-pyruvate aminotransferase; glutamic-pyruvic transaminase (GPT); alanine transaminase	3668	1186
b2291	2408862	2409461	<i>yfbR</i>	5'-nucleotidase	533	487
b2292	2411352	2409520	<i>yfbS</i>	putative transporter	2906	1823
b2293	2412089	2411439	<i>yfbT</i>	sugar phosphatase	1549	423
b2294	2412594	2412100	<i>yfbU</i>	UPF0304 family protein	1626	912
b2295	2413132	2412677	<i>yfbV</i>	UPF0208 family inner membrane protein	394	1120
b2296	2413470	2414672	<i>ackA</i>	acetate kinase A and propionate kinase 2	15078	6354
b2297	2414747	2416891	<i>pta</i>	phosphate acetyltransferase	16752	2165
b2298	2417081	2418601	<i>yfcC</i>	putative inner membrane transporter; C4-dicarboxylate anaerobic carrier family protein	240	228
b2299	2419176	2418634	<i>yfcD</i>	putative NUDIX hydrolase	2406	1360
b2300	2419788	2419234	<i>yfcE</i>	phosphodiesterase activity on bis-pNPP	1382	400
b2301	2420485	2419841	<i>yfcF</i>	glutathione S-transferase	524	313
b2302	2420621	2421268	<i>yfcG</i>	GSH-dependent disulfide bond oxidoreductase	432	255
b2303	2421325	2421687	<i>folX</i>	D-erythro-7,8-dihydroneopterin triphosphate 2'-epimerase and dihydroneopterin aldolase	1676	866
b2304	2421708	2422601	<i>yfcH</i>	putative NAD-dependent nucleotide-sugar epimerase	9051	1448
b2305	2423539	2422649	<i>yfcI</i>	transposase_31 family protein	156	700
b2306	2424509	2423736	<i>hisP</i>	histidine ABC transporter ATPase	889	735
b2307	2425233	2424517	<i>hisM</i>	histidine ABC transporter permease	279	502
b2308	2425916	2425230	<i>hisQ</i>	histidine ABC transporter permease	322	562
b2309	2426788	2426006	<i>hisJ</i>	histidine ABC transporter periplasmic binding protein	3990	5591
b2310	2427791	2427009	<i>argT</i>	lysine/arginine/ornithine transporter subunit	5252	2748
b2311	2428626	2428057	<i>ubiX</i>	3-octaprenyl-4-hydroxybenzoate carboxy-lyase	174	258
b2312	2430238	2428721	<i>purF</i>	amidophosphoribosyltransferase	2562	2159
b2313	2430763	2430275	<i>cvpA</i>	colicin V production protein	483	859
b2314	2431684	2431022	<i>dedD</i>	membrane-anchored periplasmic protein involved in septation	1178	508
b2315	2432942	2431674	<i>folC</i>	bifunctional folylpolyglutamate synthase/ dihydrofolate synthase	1639	774
b2316	2433926	2433012	<i>accD</i>	acetyl-CoA carboxylase, beta (carboxyltransferase) subunit	7127	3180
b2317	2434741	2434082	<i>dedA</i>	DedA family inner membrane protein	1479	1147
b2318	2435636	2434824	<i>truA</i>	tRNA pseudouridine(38-40) synthase	868	570
b2319	2436649	2435636	<i>usg</i>	putative semialdehyde dehydrogenase	3196	1588
b2320	2437851	2436715	<i>pdxB</i>	erythronate-4-phosphate dehydrogenase	2724	1086
b2321	2437950	2438945	<i>flk</i>	putative flagella assembly protein	908	519
b2322	2440120	2438942	<i>yfcJ</i>	putative arabinose efflux transporter	121	156
b2323	2441605	2440385	<i>fabB</i>	3-oxoacyl-[acyl-carrier-protein] synthase I	14592	2266
b2324	2441764	2443770	<i>mmC</i>	fused 5-methylaminomethyl-2-thiouridine-forming enzyme methyltransferase and FAD-dependent demodification enzyme	1069	559
b2325	2444169	2443891	<i>yfcL</i>	uncharacterized protein	761	174
b2326	2444751	2444203	<i>epmC</i>	Elongation Factor P Lys34 hydroxylase	939	493
b2327	2445560	2444751	<i>yfcA</i>	TauE/TSUP family inner membrane protein	830	292
b2328	2446384	2445560	<i>mepA</i>	murein DD-endopeptidase	1275	507
b2329	2447473	2446388	<i>aroC</i>	chorismate synthase	2366	1059

b2330	2448440	2447508	<i>prmB</i>	N5-glutamine methyltransferase	3129	1054
b2331	2448606	2449157	<i>smrB</i>	putative DNA endonuclease	771	1845
b2332	2450049	2449228	<i>yfcO</i>	DUF2544 family putative outer membrane protein	643	2067
b2333	2450590	2450051	<i>yfcP</i>	putative fimbrial-like adhesin protein	28	122
b2334	2451075	2450587	<i>yfcQ</i>	putative fimbrial-like adhesin protein	15	45
b2335	2451584	2451072	<i>yfcR</i>	putative fimbrial-like adhesin protein	19	98
b2336	2452336	2451584	<i>yfcS</i>	putative periplasmic pilin chaperone	16	54
b2339	2455646	2455083	<i>yfcV</i>	putative fimbrial-like adhesin protein	36	381
b2340	2456812	2456327	<i>sixA</i>	phosphohistidine phosphatase	2020	3811
b2341	2459159	2457015	<i>fadJ</i>	enoyl-CoA hydratase/epimerase and isomerase/3-hydroxyacyl-CoA dehydrogenase	11520	9023
b2342	2460469	2459159	<i>fadI</i>	beta-ketoacyl-CoA thiolase, anaerobic, subunit	9665	3851
b2343	2460934	2460650	<i>yfcZ</i>	UPF0381 family protein	6380	1717
b2344	2461306	2462646	<i>fadL</i>	long-chain fatty acid outer membrane transporter	21741	13351
b2345	2463012	2464070	<i>yfdF</i>	uncharacterized protein	256	704
b2346	2465007	2464252	<i>mlaA</i>	ABC transporter maintaining OM lipid asymmetry, OM lipoprotein component	3916	1944
b2347	2465301	2466233	<i>yfdC</i>	putative inner membrane protein	381	818
b2349	2466545	2467702	<i>intS</i>	CPS-53 (KpLE1) prophage; putative prophage CPS-53 integrase	283	625
b2350	2467855	2468217	<i>gtrA</i>	CPS-53 (KpLE1) prophage; bactoprenol-linked glucose translocase/flippase	253	679
b2351	2468214	2469134	<i>gtrB</i>	CPS-53 (KpLE1) prophage; bactoprenol glucosyl transferase	5497	4830
b2352	2469131	2470462	<i>gtrS</i>	serotype-specific glucosyl transferase, CPS-53 (KpLE1) prophage	4171	3460
b2354	2471517	2471077	<i>yfdK</i>	CPS-53 (KpLE1) prophage; conserved protein	29	230
b2357	2472881	2472387	<i>yfdN</i>	CPS-53 (KpLE1) prophage; uncharacterized protein	2	11
b2359	2473604	2473966	<i>yfdP</i>	CPS-53 (KpLE1) prophage; uncharacterized protein	18	76
b2360	2474032	2474856	<i>yfdQ</i>	CPS-53 (KpLE1) prophage; uncharacterized protein	103	148
b2361	2474984	2475520	<i>yfdR</i>	CPS-53 (KpLE1) prophage; conserved protein	5	66
b2362	2475511	2475873	<i>yfdS</i>	CPS-53 (KpLE1) prophage; uncharacterized protein	6	70
b2363	2475873	2476178	<i>yfdT</i>	CPS-53 (KpLE1) prophage; uncharacterized protein	10	73
b2364	2477629	2476694	<i>dsdC</i>	dsd operon activator; autorepressor	729	334
b2365	2477847	2479184	<i>dsdX</i>	D-serine transporter	808	398
b2366	2479202	2480530	<i>dsdA</i>	D-serine dehydratase	1626	547
b2367	2482176	2480638	<i>emrY</i>	putative multidrug efflux system	32	491
b2368	2483339	2482176	<i>emrK</i>	multidrug resistance efflux pump membrane fusion protein	43	371
b2369	2483755	2484369	<i>evgA</i>	response regulator in two-component regulatory system with EvgS	1553	1346
b2370	2484374	2487967	<i>evgS</i>	hybrid sensory histidine kinase in two-component regulatory system with EvgA	985	2411
b2371	2489168	2488023	<i>yfdE</i>	acetyl-CoA:oxalate CoA-transferase	24	259
b2372	2490186	2489242	<i>yfdV</i>	putative transporter	19	180
b2373	2491950	2490256	<i>oxc</i>	oxalyl CoA decarboxylase, ThDP-dependent	62	172
b2374	2493254	2492004	<i>frc</i>	formyl-CoA transferase, NAD(P)-binding	47	134
b2375	2494402	2493767	<i>yfdX</i>	uncharacterized protein	30	289
b2376	2494698	2494973	<i>ypdI</i>	putative lipoprotein involved in colanic acid biosynthesis	15	486
b2377	2495292	2495050	<i>yfdY</i>	DUF2545 family putative inner membrane protein	418	487
b2378	2495645	2496565	<i>lpxP</i>	palmitoleoyl-acyl carrier protein (ACP)-dependent acyltransferase	436	4659
b2379	2498295	2497057	<i>alaC</i>	glutamate-pyruvate aminotransferase; glutamic-pyruvic transaminase (GPT); alanine transaminase	1063	772
b2380	2498671	2500368	<i>ypdA</i>	sensor kinase regulating yhjX; pyruvate-responsive YpdAB two-component system	422	1342
b2381	2500383	2501117	<i>ypdB</i>	response regulator activating yhjX; pyruvate-responsive YpdAB two-component system	610	500
b2382	2501130	2501987	<i>ypdC</i>	putative DNA-binding protein	273	233

b2383	2504485	2501990	<i>fryA</i>	putative PTS enzyme: Hpr, enzyme I and IIA components	184	144
b2384	2505547	2504510	<i>ypdE</i>	aminopeptidase	62	34
b2385	2506632	2505547	<i>ypdF</i>	Xaa-Pro aminopeptidase	88	56
b2386	2507894	2506647	<i>fryC</i>	putative enzyme IIC component of PTS	225	67
b2387	2508242	2507916	<i>fryB</i>	putative enzyme IIB component of PTS	193	30
b2388	2509426	2508461	<i>glk</i>	glucokinase	3070	755
b2389	2509630	2510886	<i>yfeO</i>	putative ion channel protein	336	711
b2390	2511001	2511327	<i>ypeC</i>	DUF2502 family putative periplasmic protein	2232	1037
b2392	2512706	2511468	<i>mntH</i>	manganese/divalent cation transporter	1172	1110
b2393	2513042	2514244	<i>nupC</i>	nucleoside (except guanosine) transporter	6882	706
b2394	2514331	2515443	<i>insLI</i>	IS186 transposase	756	842
b2395	2517832	2515643	<i>yfeA</i>	putative diguanylate cyclase	440	922
b2398	2518467	2518811	<i>yfeC</i>	DUF1323 family putative DNA-binding protein	1694	1870
b2399	2518813	2519205	<i>yfeD</i>	DUF1323 family putative DNA-binding protein	2299	1557
b2400	2520672	2519257	<i>gltX</i>	glutamyl-tRNA synthetase	18676	3316
b2405	2522477	2521593	<i>xapR</i>	transcriptional activator of xapAB	211	520
b2406	2523985	2522729	<i>xapB</i>	xanthosine transporter	290	728
b2407	2524878	2524045	<i>xapA</i>	purine nucleoside phosphorylase 2; nicotinamide 1-beta-D-ribose synthase	24	40
b2408	2525127	2525891	<i>yfeN</i>	putative outer membrane protein	63	463
b2409	2526856	2525930	<i>yfeR</i>	transcriptional regulator of yefH	174	332
b2410	2526946	2527944	<i>yfeH</i>	putative inorganic ion transporter	2927	728
b2411	2530176	2528161	<i>ligA</i>	DNA ligase, NAD(+)-dependent	2166	679
b2412	2531233	2530247	<i>zipA</i>	FtsZ stabilizer	9090	3707
b2413	2531463	2532224	<i>cysZ</i>	sulfate transporter, sulfite inhibited	670	809
b2414	2532409	2533380	<i>cysK</i>	cysteine synthase A, O-acetylserine sulfhydrylase A subunit	82332	38738
b2415	2533764	2534021	<i>ptsH</i>	phosphohistidinoprotein-hexose phosphotransferase component of PTS system (Hpr)	9489	1820
b2416	2534066	2535793	<i>ptsI</i>	PEP-protein phosphotransferase of PTS system (enzyme I)	59667	21782
b2417	2535834	2536343	<i>crr</i>	glucose-specific enzyme IIA component of PTS	35955	14575
b2418	2537237	2536386	<i>pdxK</i>	pyridoxal-pyridoxamine kinase/hydroxymethylpyrimidine kinase	1193	263
b2419	2537342	2537716	<i>yfeK</i>	uncharacterized protein	74	1766
b2420	2537749	2538483	<i>yfeS</i>	WGR domain protein	417	2863
b2421	2539583	2538672	<i>cysM</i>	cysteine synthase B (O-acetylserine sulfhydrylase B)	2875	694
b2422	2540814	2539717	<i>cysA</i>	sulfate/thiosulfate transporter subunit	4462	1845
b2423	2541679	2540804	<i>cysW</i>	sulfate/thiosulfate ABC transporter permease	1531	1080
b2424	2542512	2541679	<i>cysU</i>	sulfate/thiosulfate ABC transporter permease	897	749
b2425	2543528	2542512	<i>cysP</i>	thiosulfate-binding protein	7094	5161
b2426	2544623	2543832	<i>ucpA</i>	furfural resistance protein, putative short-chain oxidoreductase	24140	6289
b2427	2545609	2544752	<i>murR</i>	repressor for murPQ, MurNAc 6-P inducible	306	95
b2428	2545773	2546669	<i>murQ</i>	N-acetylmuramic acid 6-phosphate (MurNAc-6-P) etherase	2420	181
b2429	2546673	2548097	<i>murP</i>	N-acetylmuramic acid permease, EIIBC component, PTS system	910	236
b2430	2548102	2549406	<i>yfeW</i>	penicillin binding protein PBP4B; weak DD-carboxypeptidase activity	801	221
b2431	2550545	2549646	<i>yfeX</i>	porphyrinogen oxidase, cytoplasmic	5782	2024
b2432	2551216	2550641	<i>yfeY</i>	RpoE-regulated lipoprotein	520	1952
b2433	2551726	2551277	<i>yfeZ</i>	inner membrane protein	64	87
b2434	2552138	2551713	<i>ypeA</i>	GNAT family putative N-acetyltransferase	167	396
b2435	2552352	2553221	<i>amiA</i>	N-acetylmuramoyl-L-alanine amidase I	769	1582
b2436	2553225	2554124	<i>hemF</i>	coproporphyrinogen III oxidase	328	322
b2437	2555182	2554130	<i>eutR</i>	eut operon transcriptional activator, AraC family	151	167

b2438	2555728	2555228	<i>eutK</i>	putative ethanol utilization carboxysome structural protein	64	31
b2439	2556400	2555741	<i>eutL</i>	putative ethanol utilization carboxysome structural protein	147	64
b2440	2557297	2556410	<i>eutC</i>	ethanolamine ammonia-lyase, small subunit (light chain)	248	131
b2441	2558679	2557318	<i>eutB</i>	ethanolamine ammonia-lyase, large subunit, heavy chain	1032	2000
b2442	2558858	2560066	<i>intZ</i>	CPZ-55 prophage; putative phage integrase	0	1
b2447	2562524	2563117	<i>yffP</i>	CPZ-55 prophage; uncharacterized protein	0	1
b2449	2563980	2564372	<i>yffR</i>	CPZ-55 prophage; uncharacterized protein	0	0
b2451	2566884	2565481	<i>eutA</i>	reactivating factor for ethanolamine ammonia lyase	12	33
b2452	2568107	2566881	<i>eutH</i>	ethanolamine transporter	24	91
b2453	2569511	2568324	<i>eutG</i>	ethanol dehydrogenase involved in ethanolamine utilization; aldehyde reductase	12	108
b2454	2570337	2569501	<i>eutJ</i>	ethanolamine utilization protein, HSP70/actin superfamily protein	8	56
b2455	2571751	2570348	<i>eutE</i>	aldehyde oxidoreductase, ethanolamine utilization protein	17	52
b2456	2572050	2571763	<i>eutN</i>	Ethanolamine catabolic microcompartment shell protein	3	17
b2457	2572450	2572157	<i>eutM</i>	ethanolamine utilization protein, putative carboxysome structural protein	37	90
b2458	2573505	2572489	<i>eutD</i>	phosphate acetyltransferase	34	44
b2459	2574305	2573502	<i>eutT</i>	cobalamin adenosyltransferase involved in ethanolamine utilization	31	54
b2460	2575003	2574302	<i>eutQ</i>	RmlC-like cupin domain protein	50	59
b2461	2575457	2574978	<i>eutP</i>	putative P-loop NTPase ethanolamine utilization protein	53	121
b2462	2575805	2575470	<i>eutS</i>	putative ethanol utilization carboxysome structural protein	11	23
b2463	2578377	2576098	<i>maeB</i>	malic enzyme: putative oxidoreductase/phosphotransacetylase	25511	2928
b2464	2578666	2579616	<i>talA</i>	transaldolase A	1525	2460
b2465	2579636	2581639	<i>tktB</i>	transketolase 2, thiamine triphosphate-binding	2219	3026
b2466	2582777	2581734	<i>ypfG</i>	DUF1176 family protein	768	1442
b2467	2583478	2582903	<i>nudK</i>	GDP-mannose pyrophosphatase	1903	1038
b2468	2585525	2583546	<i>aegA</i>	putative oxidoreductase, FeS binding subunit/NAD/FAD-binding subunit	952	467
b2469	2585731	2587431	<i>narQ</i>	sensory histidine kinase in two-component regulatory system with NarP	300	719
b2470	2587595	2590708	<i>acrD</i>	aminoglycoside/multidrug efflux system	496	840
b2471	2591247	2591603	<i>yffB</i>	putative ArsC family reductase	2195	607
b2472	2591607	2592734	<i>dapE</i>	N-succinyl-diaminopimelate deacylase	1752	703
b2473	2593770	2593072	<i>ypfH</i>	palmitoyl-CoA esterase activity, uncertain physiological substrate	1183	548
b2474	2595859	2593844	<i>tmcA</i>	elongator methionine tRNA (ac4C34) acetyltransferase	580	503
b2475	2596737	2595874	<i>ypfJ</i>	putative neutral zinc metalloproteinase	1649	1678
b2476	2597618	2596905	<i>purC</i>	phosphoribosylaminoimidazole-succinocarboxamide synthetase	1533	527
b2477	2598865	2597831	<i>bamC</i>	BamABCDE complex OM biogenesis lipoprotein	6038	2338
b2478	2599760	2598882	<i>dapA</i>	dihydrodipicolinate synthase	8496	4533
b2479	2599906	2600478	<i>gcvR</i>	transcriptional repressor, regulatory protein accessory to GcvA	1112	975
b2480	2600478	2600948	<i>bcp</i>	peroxiredoxin; thiol peroxidase, thioredoxin-dependent	3358	2240
b2481	2601201	2601818	<i>hyfA</i>	hydrogenase 4, 4Fe-4S subunit	4	21
b2482	2601818	2603836	<i>hyfB</i>	hydrogenase 4, membrane subunit	50	304
b2483	2603847	2604794	<i>hyfC</i>	hydrogenase 4, membrane subunit	68	381
b2484	2604811	2606250	<i>hyfD</i>	hydrogenase 4, membrane subunit	40	126
b2485	2606262	2606912	<i>hyfE</i>	hydrogenase 4, membrane subunit	17	57
b2486	2606917	2608497	<i>hyfF</i>	hydrogenase 4, membrane subunit	43	147
b2487	2608487	2610154	<i>hyfG</i>	hydrogenase 4, subunit	102	180
b2488	2610164	2610709	<i>hyfH</i>	hydrogenase 4, Fe-S subunit	37	56
b2489	2610706	2611464	<i>hyfI</i>	hydrogenase 4, Fe-S subunit	26	61

b2490	2611457	2611870	<i>hyfJ</i>	putative processing element hydrogenase 4	15	35
b2491	2611900	2613912	<i>hyfR</i>	hydrogenase-4 transcriptional activator	115	473
b2492	2613934	2614782	<i>focB</i>	putative formate transporter	174	364
b2493	2615881	2614820	<i>yfgO</i>	putative UPF0118 family inner membrane permease	643	426
b2494	2616094	2617557	<i>bepA</i>	OM protein maintenance and assembly metalloprotease and chaperone, periplasmic	1382	2919
b2495	2617578	2617937	<i>yfgD</i>	putative oxidoreductase	2003	1862
b2496	2618776	2618075	<i>hda</i>	ATPase regulatory factor involved in DnaA inactivation	1023	1276
b2497	2620160	2618871	<i>uraA</i>	uracil permease	5256	512
b2498	2620872	2620246	<i>upp</i>	uracil phosphoribosyltransferase	9723	1822
b2499	2621197	2622234	<i>purM</i>	phosphoribosylaminoimidazole synthetase	453	609
b2500	2622234	2622872	<i>purN</i>	phosphoribosylglycinamide formyltransferase 1	773	758
b2501	2623044	2625110	<i>ppk</i>	polyphosphate kinase, component of RNA degradosome	6449	3554
b2502	2625115	2626656	<i>ppx</i>	exopolyphosphatase	2503	1520
b2503	2628938	2626695	<i>yfgF</i>	cyclic-di-GMP phosphodiesterase, anaerobic	138	947
b2504	2629290	2629481	<i>yfgG</i>	uncharacterized protein	536	3468
b2505	2629792	2630310	<i>yfgH</i>	outer membrane integrity lipoprotein	67	459
b2506	2630326	2630865	<i>yfgI</i>	nalidixic acid resistance protein, putative periplasmic protein	119	446
b2507	2632535	2630958	<i>guaA</i>	GMP synthetase (glutamine aminotransferase)	13265	2749
b2508	2634070	2632604	<i>guaB</i>	IMP dehydrogenase	5165	2114
b2509	2634232	2635602	<i>xseA</i>	exonuclease VII, large subunit	846	3145
b2510	2635814	2635599	<i>yfgJ</i>	DUF1407 family protein	335	592
b2511	2637356	2635884	<i>der</i>	GTPase; multicopy suppressor of ftsJ	4075	2467
b2512	2638652	2637474	<i>bamB</i>	BamABCDE complex OM biogenesis lipoprotein	5900	2422
b2513	2639283	2638663	<i>yfgM</i>	ancillary SecYEG translocon subunit; putative anti-RcsB factor	1969	1028
b2514	2640575	2639301	<i>hisS</i>	histidyl tRNA synthetase	3369	2080
b2515	2641804	2640686	<i>ispG</i>	1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate synthase	4808	1961
b2516	2642844	2641831	<i>rodZ</i>	MreB assembly cytoskeletal protein	3292	2279
b2517	2644283	2643129	<i>rlmN</i>	dual specificity 23S rRNA m(2)A2503, tRNA m(2)A37 methyltransferase, SAM-dependent	2298	1306
b2518	2644864	2644433	<i>ndk</i>	multifunctional nucleoside diphosphate kinase and apyrimidinic endonuclease and 3'-phosphodiesterase	5079	1871
b2519	2647325	2645013	<i>pbpC</i>	penicillin-insensitive murein repair transglycosylase; inactive transpeptidase domain protein	235	273
b2520	2652287	2647326	<i>yfhM</i>	bacterial alpha2-macroglobulin colonization factor ECAM; anti-host protease defense factor; periplasmic inner membrane-anchored lipoprotein	8371	4803
b2521	2652494	2653339	<i>sseA</i>	3-mercaptopyruvate sulfurtransferase	20106	3837
b2522	2654933	2654157	<i>sseB</i>	rhodanase-like enzyme, sulfur transfer from thiosulfate	892	846
b2523	2656358	2655075	<i>pepB</i>	aminopeptidase B	2474	1199
b2524	2656736	2656536	<i>iscX</i>	Fe(2+) donor and activity modulator for cysteine desulfurase	776	490
b2525	2657083	2656748	<i>fdx</i>	[2Fe-2S] ferredoxin	1295	524
b2526	2658935	2657085	<i>hscA</i>	DnaK-like molecular chaperone specific for IscU	1995	1382
b2527	2659467	2658952	<i>hscB</i>	HscA co-chaperone, J domain-containing protein Hsc56; IscU-specific chaperone HscAB	287	438
b2528	2659886	2659563	<i>iscA</i>	FeS cluster assembly protein	1796	1359
b2529	2660289	2659903	<i>iscU</i>	iron-sulfur cluster assembly scaffold protein	2783	2745
b2530	2661531	2660317	<i>iscS</i>	cysteine desulfurase (tRNA sulfurtransferase), PLP-dependent	5878	4529
b2531	2662131	2661643	<i>iscR</i>	isc operon transcriptional repressor; suf operon transcriptional activator; oxidative stress- and iron starvation-inducible; autorepressor	457	1193
b2532	2663323	2662583	<i>trmJ</i>	tRNA mC32,mU32 2'-O-methyltransferase, SAM-dependent	2021	1517
b2533	2663442	2664245	<i>suhB</i>	inositol monophosphatase	1132	1399

b2534	2664390	2665244	<i>yfhR</i>	putative S9 family prolyl oligopeptidase	39	416
b2535	2665435	2666715	<i>csiE</i>	stationary phase inducible protein	3004	671
b2536	2667846	2666707	<i>hcaT</i>	putative 3-phenylpropionic transporter	432	424
b2537	2668896	2668006	<i>hcaR</i>	hca operon transcriptional regulator	1973	1686
b2538	2669032	2670393	<i>hcaE</i>	3-phenylpropionate dioxygenase, large (alpha) subunit	213	516
b2539	2670390	2670908	<i>hcaF</i>	3-phenylpropionate dioxygenase, small (beta) subunit	50	147
b2540	2670908	2671228	<i>hcaC</i>	3-phenylpropionate dioxygenase, ferredoxin subunit	16	34
b2541	2671225	2672037	<i>hcaB</i>	2,3-dihydroxy-2,3-dihydrophenylpropionate dehydrogenase	51	68
b2542	2672047	2673249	<i>hcaD</i>	phenylpropionate dioxygenase, ferredoxin reductase subunit	161	239
b2543	2673346	2673768	<i>yphA</i>	DoxX family inner membrane protein	356	194
b2544	2674688	2673816	<i>yphB</i>	mutarotase superfamily protein, YphB family	85	164
b2545	2675761	2674700	<i>yphC</i>	putative Zn-dependent NAD(P)-binding oxidoreductase	100	119
b2546	2676825	2675827	<i>yphD</i>	putative sugar ABC transporter permease	21	83
b2547	2678361	2676850	<i>yphE</i>	putative sugar ABC transporter ATPase	87	203
b2548	2679367	2678384	<i>yphF</i>	putative sugar ABC transporter periplasmic binding protein	79	167
b2549	2682745	2679464	<i>yphG</i>	DUF4380 domain-containing TPR repeat protein	111	240
b2550	2682863	2684056	<i>yphH</i>	putative DNA-binding transcriptional regulator	220	722
b2551	2685507	2684254	<i>glyA</i>	serine hydroxymethyltransferase	32517	4060
b2552	2685835	2687025	<i>hmp</i>	fused nitric oxide dioxygenase/dihydropteridine reductase 2	1294	468
b2553	2687408	2687070	<i>glnB</i>	regulatory protein P-II for glutamine synthetase	771	712
b2554	2688803	2687469	<i>glrR</i>	response regulator regulating glmY sRNA in two-component system with sensor protein GlrK	405	281
b2555	2689506	2688793	<i>yfhG</i>	putative outer membrane protein modulating the QseEF response	365	373
b2556	2691098	2689671	<i>glrK</i>	sensor protein kinase regulating glmY sRNA in two-component system with response regulator GlrR	472	994
b2557	2695543	2691656	<i>purL</i>	phosphoribosylformyl-glycineamide synthetase	1721	1235
b2558	2695801	2697357	<i>mltF</i>	membrane-bound lytic transglycosylase F, murein hydrolase	198	1086
b2559	2697857	2697354	<i>tadA</i>	tRNA-specific adenosine deaminase	197	235
b2560	2698550	2697915	<i>pgpC</i>	phosphatidylglycerophosphatase C, membrane bound	381	469
b2561	2698759	2699607	<i>yfhH</i>	putative DNA-binding transcriptional regulator	475	432
b2562	2699663	2699923	<i>yfhL</i>	putative 4Fe-4S cluster-containing protein	95	445
b2563	2700998	2700618	<i>acpS</i>	holo-[acyl-carrier-protein] synthase 1	851	456
b2564	2701729	2700998	<i>pdxJ</i>	pyridoxine 5'-phosphate synthase	1919	599
b2565	2702469	2701741	<i>recO</i>	gap repair protein	345	187
b2566	2703386	2702481	<i>era</i>	membrane-associated, 16S rRNA-binding GTPase	2429	1966
b2567	2704063	2703383	<i>rnc</i>	RNase III	1058	1646
b2568	2705309	2704335	<i>lepB</i>	leader peptidase (signal peptidase I)	4377	2813
b2569	2707124	2705325	<i>lepA</i>	back-translocating elongation factor EF4, GTPase	5164	3150
b2570	2707801	2707322	<i>rseC</i>	SoxR iron-sulfur cluster reduction factor component	324	356
b2571	2708754	2707798	<i>rseB</i>	anti-sigma E factor, binds RseA	2466	3495
b2572	2709404	2708754	<i>rseA</i>	anti-sigma factor	6840	16299
b2573	2710012	2709437	<i>rpoE</i>	RNA polymerase sigma E factor	1827	3605
b2574	2710420	2712042	<i>nadB</i>	quinolinate synthase, L-aspartate oxidase (B protein) subunit	153	1202
b2575	2712764	2712027	<i>trmN</i>	tRNA1(Val) (adenine(37)-N6)-methyltransferase	255	451
b2576	2712896	2714230	<i>srmB</i>	ATP-dependent RNA helicase	1627	901
b2577	2715320	2714439	<i>yfiE</i>	putative DNA-binding transcriptional regulator	500	485
b2578	2715423	2716010	<i>eamB</i>	cysteine and O-acetylserine exporter	83	299
b2579	2716449	2716066	<i>grcA</i>	autonomous glycyl radical cofactor	20676	40007
b2580	2716754	2717443	<i>ung</i>	uracil-DNA-glycosylase	946	704
b2581	2718528	2717491	<i>yfiF</i>	putative methyltransferase	5473	1418

b2582	2718735	2719154	<i>trxC</i>	thioredoxin 2	1937	3451
b2583	2719223	2719921	<i>yfiP</i>	DTW domain protein	185	201
b2584	2719953	2722613	<i>pka</i>	protein lysine acetyltransferase	15460	4238
b2585	2722727	2724082	<i>pssA</i>	phosphatidylserine synthase; CDP-diacylglycerol-serine O-phosphatidyltransferase	6712	5378
b2586	2724128	2724451	<i>yfiM</i>	putative lipoprotein	477	701
b2587	2725746	2724448	<i>kgtP</i>	alpha-ketoglutarate transporter	14074	11133
b2592	2734173	2731600	<i>clpB</i>	protein disaggregation chaperone	48432	23035
b2593	2735034	2734303	<i>yfiH</i>	UPF0124 family protein	539	227
b2594	2736011	2735031	<i>rluD</i>	23S rRNA pseudouridine(1911,1915,1917) synthase	1364	1327
b2595	2736146	2736883	<i>bamD</i>	BamABCDE complex OM biogenesis lipoprotein	5344	6305
b2597	2737154	2737495	<i>raiA</i>	cold shock protein associated with 30S ribosomal subunit	279411	425157
b2599	2737745	2738905	<i>pheA</i>	chorismate mutase and prephenate dehydratase, P-protein	2447	4733
b2600	2740069	2738948	<i>tyrA</i>	fused chorismate mutase T/prephenate dehydrogenase	947	515
b2601	2741150	2740080	<i>aroF</i>	3-deoxy-D-arabino-heptulosonate-7-phosphate synthase, tyrosine-repressible	1408	1003
b2602	2741360	2741725	<i>yfiL</i>	lipoprotein	156	822
b2603	2741875	2742393	<i>yfiR</i>	putative periplasmic inhibitor of YfiN activity	346	1151
b2604	2742383	2743609	<i>yfiN</i>	putative membrane-anchored diguanylate cyclase	373	818
b2605	2743625	2744107	<i>yfiB</i>	OM lipoprotein putative positive effector of YfiN activity	1007	530
b2606	2744530	2744183	<i>rplS</i>	50S ribosomal subunit protein L19	25278	7633
b2607	2745339	2744572	<i>trmD</i>	tRNA m(1)G37 methyltransferase, SAM-dependent	29919	8073
b2608	2745918	2745370	<i>rimM</i>	ribosome maturation factor	25093	7569
b2609	2746185	2745937	<i>rpsP</i>	30S ribosomal subunit protein S16	4007	1489
b2610	2747795	2746434	<i>ffh</i>	Signal Recognition Particle (SRP) component with 4.5S RNA (ffs)	3198	2123
b2611	2747962	2748753	<i>ypjD</i>	cytochrome c assembly protein family inner membrane protein	509	529
b2614	2750708	2750115	<i>grpE</i>	heat shock protein	18413	10525
b2615	2750831	2751709	<i>nadK</i>	NAD kinase	1263	1259
b2616	2751795	2753456	<i>recN</i>	recombination and repair protein	2394	5845
b2617	2753605	2753946	<i>bamE</i>	lipoprotein component of BamABCDE OM biogenesis complex	5535	26307
b2618	2754298	2754008	<i>ratB</i>	UPF0125 family protein	528	526
b2619	2754764	2754288	<i>ratA</i>	toxic UPF0083 family protein inhibitor of 70S ribosome formation	882	516
b2620	2754896	2755378	<i>smpB</i>	tmRNA-binding trans-translation protein	1794	1928
b2622	2756159	2757400	<i>intA</i>	CP4-57 prophage; integrase	1409	833
b2623	2758600	2757644	<i>yfiH</i>	CP4-57 prophage; uncharacterized protein	510	933
b2624	2758644	2758856	<i>alpA</i>	CP4-57 prophage; DNA-binding transcriptional activator	10	16
b2625	2758985	2760394	<i>yfiI</i>	CP4-57 prophage; uncharacterized protein	294	2218
b2626	2760547	2761173	<i>yfiJ</i>	CP4-57 prophage; uncharacterized protein	28	154
b2627	2763540	2761351	<i>yfiK</i>	radiation resistance protein; DEAD/H helicase-like protein; CP4-57 putative defective prophage	1732	1067
b2628	2765153	2763537	<i>yfiL</i>	CP4-57 putative defective prophage, DUF4297/DUF1837 polymorphic toxin family protein	2538	2281
b2629	2765776	2765513	<i>yfiM</i>	CP4-57 prophage; uncharacterized protein	19	152
b2630	2765918	2766991	<i>rnlA</i>	CP4-57 prophage; RNase LS	2682	61380
b2631	2766984	2767355	<i>rnlB</i>	CP4-57 prophage; uncharacterized protein	399	1555
b2632	2767710	2768573	<i>yfiP</i>	CP4-57 prophage; 50S ribosome-binding GTPase family protein	54	79
b2633	2768665	2769486	<i>yfiQ</i>	CP4-57 prophage; uncharacterized protein	48	575
b2634	2769703	2770404	<i>yfiR</i>	CP4-57 prophage; putative DNA-binding transcriptional regulator	23	56
b2635	2770445	2770681	<i>ypjK</i>	CP4-57 prophage; putative inner membrane protein	14	29
b2636	2770681	2771124	<i>yfiS</i>	CP4-57 prophage; uncharacterized protein	23	27
b2637	2771148	2771615	<i>yfiT</i>	CP4-57 prophage; putative periplasmic protein	94	75

b2642	2773318	2775021	<i>yjfW</i>	CP4-57 prophage; putative inner membrane protein	813	3639
b2643	2775919	2776377	<i>yjfX</i>	CP4-57 prophage; putative antirestriction protein	29	64
b2644	2776386	2776868	<i>yjfY</i>	CP4-57 prophage; putative DNA repair protein	9	17
b2645	2777115	2777432	<i>yjfZ</i>	CP4-57 prophage; antitoxin of the YpjF-YfjZ toxin-antitoxin system	8	16
b2646	2777453	2777782	<i>ypjF</i>	CP4-57 prophage; toxin of the YpjF-YfjZ toxin-antitoxin system	19	27
b2647	2782726	2778146	<i>ypjA</i>	adhesin-like autotransporter	529	5436
b2659	2788985	2789962	<i>csiD</i>	carbon starvation protein	4670	608
b2660	2789982	2791250	<i>lhgO</i>	L-2-hydroxyglutarate oxidase	1966	327
b2661	2791273	2792721	<i>gabD</i>	succinate-semialdehyde dehydrogenase I, NADP-dependent	1536	246
b2662	2792735	2794015	<i>gabT</i>	4-aminobutyrate aminotransferase, PLP-dependent	1298	257
b2663	2794253	2795653	<i>gabP</i>	gamma-aminobutyrate transporter	324	267
b2664	2795674	2796336	<i>csiR</i>	transcriptional repressor of <i>csiD</i>	296	489
b2665	2796786	2796337	<i>ygaU</i>	uncharacterized protein	2191	3066
b2666	2797028	2796870	<i>yqaE</i>	cyaR sRNA-regulated protein	200	690
b2667	2797211	2797510	<i>ygaV</i>	tributyltin-inducible repressor of <i>ygaVP</i>	39	455
b2668	2797520	2798044	<i>ygaP</i>	DUF2892 family inner membrane rhodanese	131	323
b2669	2798495	2798091	<i>stpA</i>	DNA binding protein, nucleoid-associated	46	221
b2670	2799164	2799613	<i>alaE</i>	alanine exporter, alanine-inducible, stress-responsive	3478	6097
b2671	2799994	2799650	<i>ygaC</i>	uncharacterized protein	1049	1340
b2672	2800146	2800475	<i>ygaM</i>	putative membrane-anchored DUF883 family ribosome-binding protein	1914	2151
b2673	2800723	2800968	<i>nrdH</i>	hydrogen donor for NrdEF electron transport system; glutaredoxin-like protein	55	80
b2674	2800965	2801375	<i>nrdI</i>	NrdEF cluster assembly flavodoxin	73	86
b2675	2801348	2803492	<i>nrdE</i>	ribonucleoside-diphosphate reductase 2, alpha subunit	334	501
b2676	2803502	2804461	<i>nrdF</i>	ribonucleoside-diphosphate reductase 2, beta subunit, ferritin-like protein	169	311
b2677	2804815	2806017	<i>proV</i>	glycine betaine/proline ABC transporter periplasmic binding protein	139	1462
b2678	2806010	2807074	<i>proW</i>	glycine betaine/proline ABC transporter permease	39	76
b2679	2807132	2808124	<i>proX</i>	glycine betaine/proline ABC transporter periplasmic binding protein; cold shock protein	84	263
b2682	2809617	2810354	<i>ygaZ</i>	putative L-valine exporter, norvaline resistance protein	311	783
b2683	2810344	2810679	<i>ygaH</i>	putative L-valine exporter, norvaline resistance protein	87	150
b2684	2810770	2811300	<i>mprA</i>	transcriptional repressor of microcin B17 synthesis and multidrug efflux	1473	1873
b2685	2811427	2812599	<i>emrA</i>	multidrug efflux system	1291	827
b2686	2812616	2814154	<i>emrB</i>	multidrug efflux system protein	646	317
b2687	2814733	2814218	<i>luxS</i>	S-ribosylhomocysteine lyase	7245	2308
b2688	2816439	2814883	<i>gshA</i>	glutamate-cysteine ligase	5518	3235
b2689	2816940	2816512	<i>yqaA</i>	COG1238 family inner membrane protein	244	223
b2690	2817503	2816937	<i>yqaB</i>	fructose-1-P and 6-phosphogluconate phosphatase	970	633
b2696	2819146	2818961	<i>csrA</i>	pleiotropic regulatory protein for carbon source metabolism	7517	5599
b2697	2822011	2819381	<i>alaS</i>	alanyl-tRNA synthetase	20710	10198
b2698	2822639	2822139	<i>recX</i>	regulatory protein for RecA	75	110
b2699	2823769	2822708	<i>recA</i>	DNA recombination and repair protein; ssDNA-dependent ATPase; synaptase; ssDNA and dsDNA binding protein; ATP-dependent homologous DNA strand exchanger; recombinase A; LexA autocleavage cofactor	17823	6682
b2700	2824346	2823849	<i>pncC</i>	nicotinamide-nucleotide amidohydrolase; NMN amidohydrolase	565	220
b2701	2825576	2824491	<i>mltB</i>	membrane-bound lytic murein transglycosylase B	854	467
b2702	2825832	2826395	<i>srlA</i>	glucitol/sorbitol-specific enzyme IIC component of PTS	882	47
b2703	2826392	2827351	<i>srlE</i>	glucitol/sorbitol-specific enzyme IIB component of PTS	850	157

b2704	2827362	2827733	<i>srlB</i>	glucitol/sorbitol-specific enzyme IIA component of PTS	156	9
b2705	2827737	2828516	<i>srlD</i>	sorbitol-6-phosphate dehydrogenase	729	67
b2706	2828621	2828980	<i>srlM</i>	sorbitol=responsive srl operon transcriptional activator	116	46
b2707	2829047	2829820	<i>srlR</i>	sorbitol-inducible srl operon transcriptional repressor	3612	490
b2708	2829813	2830778	<i>srlQ</i>	D-arabinose 5-phosphate isomerase	1841	101
b2709	2832289	2830775	<i>norR</i>	anaerobic nitric oxide reductase DNA-binding transcriptional activator	145	189
b2710	2832476	2833915	<i>norV</i>	anaerobic nitric oxide reductase flavorubredoxin	108	279
b2711	2833912	2835045	<i>norW</i>	NADH:flavorubredoxin oxidoreductase	41	77
b2712	2837425	2835173	<i>hypF</i>	carbamoyl phosphate phosphatase and [NiFe] hydrogenase maturation protein	705	819
b2713	2838105	2837578	<i>hydN</i>	formate dehydrogenase-H, [4Fe-4S] ferredoxin subunit	44	115
b2714	2839264	2838254	<i>ascG</i>	asc operon transcriptional repressor; prpBC operon repressor	408	412
b2715	2839524	2840981	<i>ascF</i>	cellobiose/arbutin/salicin-specific PTS enzymes, IIB and IC components	67	94
b2716	2840990	2842414	<i>ascB</i>	cryptic 6-phospho-beta-glucosidase	323	437
b2717	2843043	2842573	<i>hycI</i>	protease involved in processing C-terminal end of HycE	1600	511
b2718	2843446	2843036	<i>hycH</i>	hydrogenase 3 maturation protein	28	36
b2719	2844210	2843443	<i>hycG</i>	hydrogenase 3 and formate hydrogenase complex, HycG subunit	32	53
b2720	2844752	2844210	<i>hycF</i>	formate hydrogenlyase complex iron-sulfur protein	15	9
b2721	2846471	2844762	<i>hycE</i>	hydrogenase 3, large subunit	29	66
b2722	2847412	2846489	<i>hycD</i>	hydrogenase 3, membrane subunit	10	34
b2723	2849241	2847415	<i>hycC</i>	hydrogenase 3, membrane subunit	15	32
b2724	2849849	2849238	<i>hycB</i>	hydrogenase 3, Fe-S subunit	4	6
b2725	2850435	2849974	<i>hycA</i>	regulator of the transcriptional regulator FhlA	7	18
b2726	2850647	2850997	<i>hypA</i>	protein involved in nickel insertion into hydrogenases 3	1883	996
b2727	2851001	2851873	<i>hypB</i>	GTP hydrolase involved in nickel liganding into hydrogenases	5085	386
b2728	2851864	2852136	<i>hypC</i>	hydrogenase maturation protein	718	54
b2729	2852136	2853257	<i>hypD</i>	hydrogenase maturation protein	2061	286
b2730	2853254	2854264	<i>hypE</i>	carbamoyl dehydratase, hydrogenases 1,2,3 maturation protein	1330	155
b2731	2854338	2856416	<i>fhlA</i>	formate hydrogenlyase transcriptional activator	558	629
b2732	2856806	2856453	<i>ygbA</i>	uncharacterized protein	64	111
b2733	2857093	2859654	<i>mutS</i>	methyl-directed mismatch repair protein	2075	696
b2734	2859760	2860416	<i>pphB</i>	serine/threonine-specific protein phosphatase 2	59	180
b2735	2861234	2860467	<i>ygbI</i>	DeoR family putative transcriptional regulator	1091	1747
b2736	2861430	2862338	<i>ygbJ</i>	putative dehydrogenase	38	134
b2737	2862335	2863501	<i>ygbK</i>	FliA-regulated DUF1537 family protein	79	103
b2738	2863593	2864231	<i>ygbL</i>	putative class II aldolase	33	55
b2739	2864236	2865012	<i>ygbM</i>	putative hydroxypyruvate isomerase	55	112
b2740	2865101	2866465	<i>ygbN</i>	putative transporter	70	372
b2741	2867551	2866559	<i>rpoS</i>	RNA polymerase, sigma S (sigma 38) factor	15977	12601
b2742	2868753	2867614	<i>nlpD</i>	activator of AmiC murein hydrolase activity, lipoprotein	12248	14351
b2743	2869519	2868893	<i>pcm</i>	L-isoaspartate protein carboxylmethyltransferase type II	1079	765
b2744	2870274	2869513	<i>umpG</i>	broad specificity 5'(3')-nucleotidase and polyphosphatase	1251	426
b2745	2871304	2870255	<i>truD</i>	tRNA(Glu) pseudouridine(13) synthase	2091	932
b2746	2871780	2871301	<i>ispF</i>	2C-methyl-D-erythritol 2,4-cyclodiphosphate synthase	483	167
b2747	2872490	2871780	<i>ispD</i>	4-diphosphocytidyl-2C-methyl-D-erythritol synthase	374	170
b2748	2872820	2872509	<i>ftsB</i>	cell division protein	434	576
b2749	2873337	2873014	<i>ygbE</i>	DUF3561 family inner membrane protein	86	463
b2750	2873992	2873387	<i>cysC</i>	adenosine 5'-phosphosulfate kinase	716	224
b2751	2875419	2873992	<i>cysN</i>	sulfate adenylyltransferase, subunit 1	8282	1862
b2752	2876329	2875421	<i>cysD</i>	sulfate adenylyltransferase, subunit 2	6158	2534

b2753	2876581	2877618	<i>iap</i>	aminopeptidase in alkaline phosphatase isozyme conversion	1119	664
b2754	2878853	2878569	<i>ygbF</i>	CRISPR adaptation ssRNA endonuclease	48	872
b2755	2879772	2878855	<i>ygbT</i>	multifunctional endonuclease CasI, CRISPR adaptation protein; DNA repair enzyme	146	171
b2756	2880387	2879788	<i>casE</i>	CRISPR RNA precursor cleavage enzyme; CRISP RNA (crRNA) containing Cascade antiviral complex protein	189	313
b2757	2881048	2880374	<i>casD</i>	CRISP RNA (crRNA) containing Cascade antiviral complex protein	167	222
b2758	2882142	2881051	<i>casC</i>	CRISP RNA (crRNA) containing Cascade antiviral complex protein	257	373
b2759	2882637	2882155	<i>casB</i>	CRISP RNA (crRNA) containing Cascade antiviral complex protein	130	95
b2760	2884138	2882630	<i>casA</i>	CRISP RNA (crRNA) containing Cascade antiviral complex protein	169	367
b2761	2887219	2884553	<i>ygcB</i>	Cascade complex anti-viral R-loop helicase-annealase Cas3	5460	1437
b2762	2888312	2887578	<i>cysH</i>	phosphoadenosine phosphosulfate reductase; PAPS reductase, thioredoxin dependent	8256	2176
b2763	2890099	2888387	<i>cysI</i>	sulfite reductase, beta subunit, NAD(P)-binding, heme-binding	9416	2257
b2764	2891898	2890099	<i>cysJ</i>	sulfite reductase, alpha subunit, flavoprotein	6191	1677
b2765	2892214	2892579	<i>queD</i>	6-pyruvoyl tetrahydrobiopterin synthase (PTPS)	292	408
b2766	2892657	2893928	<i>ygcN</i>	putative oxidoreductase	557	175
b2767	2893919	2894179	<i>ygcO</i>	putative 4Fe-4S cluster-containing protein	45	17
b2768	2894196	2894771	<i>ygcP</i>	putative antiterminator regulatory protein	350	125
b2769	2895779	2894919	<i>ygcQ</i>	putative flavoprotein	21	129
b2770	2896555	2895776	<i>ygcR</i>	putative flavoprotein	11	30
b2771	2897870	2896533	<i>ygcS</i>	putative MFS sugar transporter; membrane protein	16	73
b2774	2900273	2899488	<i>ygcW</i>	putative SDR family oxidoreductase	29	63
b2775	2900592	2901869	<i>yqcE</i>	putative MFS transporter, inner membrane protein	133	228
b2776	2901896	2903374	<i>ygcE</i>	putative kinase	176	372
b2777	2905418	2904747	<i>queE</i>	7-carboxy-7-deazaguanine synthase; queosine biosynthesis	545	750
b2778	2905711	2906583	<i>ygcG</i>	TPM domain protein, putative phosphatase	36	415
b2779	2907941	2906643	<i>eno</i>	enolase	75596	11853
b2780	2909666	2908029	<i>pyrG</i>	CTP synthetase	14589	4516
b2781	2910685	2909894	<i>mazG</i>	nucleoside triphosphate pyrophosphohydrolase	986	749
b2782	2911091	2910756	<i>mazF</i>	mRNA interferase toxin, antitoxin is MazE	200	306
b2783	2911339	2911091	<i>mazE</i>	antitoxin of the ChpA-ChpR toxin-antitoxin system	245	869
b2784	2913651	2911417	<i>relA</i>	(p)ppGpp synthetase I/GTP pyrophosphokinase	640	414
b2785	2915000	2913699	<i>rlmD</i>	23S rRNA m(5)U1939 methyltransferase, SAM-dependent	1024	845
b2786	2915057	2917813	<i>barA</i>	hybrid sensory histidine kinase, in two-component regulatory system with UvrY	875	975
b2787	2919385	2918045	<i>gudD</i>	D-glucarate dehydratase 1	412	250
b2788	2920746	2919406	<i>gudX</i>	glucarate dehydratase-related protein, substrate unknown	184	141
b2789	2922100	2920748	<i>gudP</i>	putative D-glucarate transporter	554	247
b2790	2922984	2922535	<i>yqcA</i>	short-chain flavodoxin, FMN-binding	1146	455
b2791	2923784	2923002	<i>truC</i>	tRNA(Ile1,Asp) pseudouridine(65) synthase	328	246
b2792	2924113	2923784	<i>yqcC</i>	DUF446 family protein	136	146
b2793	2925280	2924735	<i>syd</i>	SecY-interacting protein	577	876
b2794	2925348	2926196	<i>queF</i>	7-cyano-7-deazaguanine reductase (NADPH-dependent)	1101	1255
b2795	2926308	2927672	<i>ygdH</i>	UPF0717 family protein	17044	3096
b2796	2928229	2929518	<i>sdaC</i>	putative serine transporter	10495	1059
b2797	2929576	2930943	<i>sdaB</i>	L-serine dehydratase 2	2907	308
b2798	2931055	2931810	<i>ygdG</i>	Ssb-binding protein, misidentified as ExoIX	384	191
b2799	2933013	2931865	<i>fucO</i>	L-1,2-propanediol oxidoreductase	2146	635
b2800	2933688	2933041	<i>fucA</i>	L-fucose-1-phosphate aldolase	411	132

b2801	2934235	2935551	<i>fucP</i>	L-fucose transporter	1215	946
b2802	2935584	2937359	<i>fucI</i>	L-fucose isomerase	1656	260
b2803	2937468	2938886	<i>fucK</i>	L-fuculokinase	806	359
b2804	2938888	2939310	<i>fucU</i>	L-fucose mutarotase	355	283
b2805	2939368	2940099	<i>fucR</i>	l-fucose operon activator	2160	1404
b2806	2941243	2940143	<i>rlmM</i>	23S rRNA C2498 2'-O-ribose methyltransferase, SAM-dependent	776	636
b2807	2941631	2941236	<i>ygdD</i>	UPF0382 family inner membrane protein	102	67
b2808	2942567	2941650	<i>gcvA</i>	glycine cleavage system transcriptional activator; autorepressor	442	1250
b2809	2943145	2942918	<i>ygdI</i>	DUF903 family verified lipoprotein	1386	2273
b2810	2943337	2944542	<i>csdA</i>	cysteine sulfinate desulfinate	654	684
b2811	2944542	2944985	<i>csdE</i>	CsdA-binding activator; Fe-S protein	476	295
b2812	2945842	2945036	<i>tcdA</i>	tRNA threonylcarbamoyladenine dehydratase; sulfur acceptor for CsdA	210	235
b2813	2947178	2946081	<i>mltA</i>	membrane-bound lytic murein transglycosylase A	764	861
b2817	2949010	2947757	<i>amiC</i>	N-acetylmuramoyl-L-alanine amidase	505	1099
b2818	2949242	2950573	<i>argA</i>	amino acid N-acetyltransferase and inactive acetylglutamate kinase	140	2931
b2819	2952461	2950635	<i>recD</i>	exonuclease V (RecBCD complex), alpha chain	675	767
b2820	2956003	2952461	<i>recB</i>	exonuclease V (RecBCD complex), beta subunit	1121	1850
b2821	2958884	2955996	<i>ptrA</i>	protease III	1141	4682
b2822	2962428	2959060	<i>recC</i>	exonuclease V (RecBCD complex), gamma chain	1141	2050
b2823	2962764	2962441	<i>ppdC</i>	putative prepilin peptidase-dependent protein	76	292
b2824	2963156	2962749	<i>ygdB</i>	DUF2509 family protein	36	64
b2825	2963716	2963153	<i>ppdB</i>	putative prepilin peptidase-dependent protein	95	197
b2826	2964177	2963707	<i>ppdA</i>	putative prepilin peptidase-dependent protein	177	198
b2827	2965155	2964361	<i>thyA</i>	thymidylate synthetase	2168	1241
b2828	2966037	2965162	<i>lgt</i>	phosphatidylglycerol-prolipoprotein diacylglycerol transferase	863	674
b2829	2968434	2966188	<i>ptsP</i>	PEP-protein phosphotransferase enzyme I; GAF domain containing protein	3806	2613
b2830	2968977	2968447	<i>rppH</i>	RNA pyrophosphohydrolase	2147	4098
b2831	2969662	2970351	<i>mutH</i>	methyl-directed mismatch repair protein	122	287
b2832	2970420	2971133	<i>ygdQ</i>	UPF0053 family inner membrane protein	182	489
b2833	2971271	2971489	<i>ygdR</i>	DUF903 family verified lipoprotein	4263	5886
b2834	2971597	2972637	<i>tas</i>	putative NADP(H)-dependent aldo-keto reductase	3092	1517
b2835	2973862	2972669	<i>lplT</i>	lysophospholipid transporter	281	225
b2836	2976014	2973855	<i>aas</i>	fused 2-acylglycerophospho-ethanolamine acyl transferase/acyl-acyl carrier protein synthetase	1239	949
b2837	2976599	2977630	<i>galR</i>	galactose-inducible d-galactose regulon transcriptional repressor; autorepressor	1022	806
b2838	2978899	2977637	<i>lysA</i>	diaminopimelate decarboxylase, PLP-binding	723	470
b2839	2979021	2979956	<i>lysR</i>	transcriptional activator of lysA; autorepressor	244	269
b2840	2980635	2979943	<i>ygeA</i>	Asp/Glu_racemase family protein	487	744
b2841	2982182	2980764	<i>araE</i>	arabinose transporter	238	415
b2842	2983258	2982497	<i>kduD</i>	2-dehydro-3-deoxy-D-gluconate 5-dehydrogenase; KDG oxidoreductase; 20-ketosteroid reductase	381	277
b2843	2984124	2983288	<i>kduI</i>	hexuronate isomerase	423	249
b2844	2985592	2984411	<i>yqeF</i>	short chain acyltransferase	4194	894
b2845	2985847	2987076	<i>yqeG</i>	putative transporter	598	499
b2846	2987536	2988168	<i>yqeH</i>	putative LuxR family transcriptional regulator	54	338
b2847	2988502	2989311	<i>yqeI</i>	putative transcriptional regulator	54	658
b2848	2989304	2989786	<i>yqeJ</i>	uncharacterized protein	15	397
b2849	2990360	2989935	<i>yqeK</i>	uncharacterized protein	1	43
b2851	2991268	2991759	<i>ygeG</i>	SycD-like chaperone family TPR-repeat-containing protein	7	173

b2852	2992094	2993470	<i>ygeH</i>	putative transcriptional regulator	16	605
b2853	2993638	2993856	<i>ygeI</i>	uncharacterized protein	9	126
b2860	2997277	2996372	<i>insD1</i>	IS2 transposase TnpB	652	819
b2861	2997600	2997235	<i>insC1</i>	IS2 repressor TnpA	403	429
b2865	2999891	2999136	<i>ygeR</i>	LysM domain-containing M23 family putative peptidase; septation lipoprotein	1034	1245
b2866	3000345	3002603	<i>xdhA</i>	xanthine dehydrogenase, molybdenum binding subunit	525	1381
b2867	3002614	3003492	<i>xdhB</i>	xanthine dehydrogenase, FAD-binding subunit	121	301
b2868	3003489	3003968	<i>xdhC</i>	xanthine dehydrogenase, Fe-S binding subunit	106	370
b2869	3005786	3004008	<i>ygeV</i>	putative sigma-54-interacting transcriptional activator	13111	7564
b2870	3006262	3007452	<i>ygeW</i>	putative carbamoyltransferase	374	4699
b2871	3007510	3008706	<i>ygeX</i>	2,3-diaminopropionate ammonia lyase, PLP-dependent	145	1047
b2872	3008764	3009975	<i>ygeY</i>	putative peptidase	173	2870
b2873	3010028	3011413	<i>hyuA</i>	D-stereospecific phenylhydantoinase	47	601
b2874	3011461	3012393	<i>yqeA</i>	putative amino acid kinase	126	413
b2875	3014239	3012614	<i>yqeB</i>	XdhC-CoxI family protein with NAD(P)-binding Rossmann fold	2313	1735
b2876	3015057	3014287	<i>yqeC</i>	putative selenium-dependent hydroxylase accessory protein	1733	695
b2877	3015160	3015738	<i>mocA</i>	CTP:molybdopterin cytidyltransferase	3717	4051
b2878	3016060	3019158	<i>ygfK</i>	putative Fe-S subunit oxidoreductase subunit	592	2517
b2879	3019161	3020489	<i>ssnA</i>	putative chlorohydrolase/aminohydrolase	69	343
b2880	3020540	3021319	<i>ygfM</i>	putative oxidoreductase	82	356
b2881	3021316	3024186	<i>xdhD</i>	putative hypoxanthine oxidase, molybdopterin-binding/Fe-S binding	415	1499
b2882	3024351	3025751	<i>xanQ</i>	xanthine permease	117	807
b2883	3025766	3027085	<i>guaD</i>	guanine deaminase	220	610
b2886	3029012	3028524	<i>ygfS</i>	putative 4Fe-4S ferredoxin-type oxidoreductase subunit	19	65
b2887	3030931	3029012	<i>ygfT</i>	putative oxidoreductase, Fe-S subunit/nucleotide-binding subunit	60	447
b2888	3031367	3032815	<i>uacT</i>	uric acid permease	46	615
b2889	3033065	3033613	<i>idi</i>	isopentenyl diphosphate isomerase	1138	1415
b2890	3035174	3033657	<i>lysS</i>	lysine tRNA synthetase, constitutive	9886	2268
b2891	3036282	3035184	<i>prfB</i>	peptide chain release factor RF-2	4853	1940
b2892	3038106	3036373	<i>recJ</i>	ssDNA exonuclease, 5' --> 3'-specific	1016	613
b2893	3038822	3038112	<i>dsbC</i>	protein disulfide isomerase II	1407	1769
b2894	3039743	3038847	<i>xerD</i>	site-specific tyrosine recombinase	765	1353
b2895	3039855	3040376	<i>fldB</i>	flavodoxin 2	1217	1663
b2896	3040823	3040416	<i>cptA</i>	toxin of CptAB toxin-antitoxin pair	1000	551
b2897	3041070	3040804	<i>sdhE</i>	flavinator of succinate dehydrogenase; antitoxin of CptAB toxin-antitoxin pair	1476	1152
b2898	3041313	3042293	<i>ygfZ</i>	iron-sulfur cluster repair protein, plumbagin resistance	4292	2064
b2899	3043148	3042489	<i>yqfA</i>	hemolysin III family HylIII inner membrane protein	4191	4535
b2900	3043623	3043312	<i>yqfB</i>	UPF0267 family protein	595	855
b2901	3043662	3045101	<i>bglA</i>	6-phospho-beta-glucosidase A	3741	2048
b2902	3045901	3045158	<i>ygfF</i>	putative NAD(P)-dependent oxidoreductase	181	155
b2903	3049041	3046168	<i>gcvP</i>	glycine decarboxylase, PLP-dependent, subunit P of glycine cleavage complex	10238	1842
b2904	3049549	3049160	<i>gcvH</i>	glycine cleavage complex lipoylprotein	5783	2012
b2905	3050667	3049573	<i>gcvT</i>	aminomethyltransferase, tetrahydrofolate-dependent, subunit (T protein) of glycine cleavage complex	9651	1151
b2906	3052317	3051115	<i>ubiI</i>	2-octaprenylphenol hydroxylase, FAD-dependent	1075	481
b2907	3053518	3052340	<i>ubiH</i>	2-octaprenyl-6-methoxyphenol hydroxylase, FAD/NAD(P)-binding	815	397
b2908	3054840	3053515	<i>pepP</i>	proline aminopeptidase P II	5814	2223
b2909	3055444	3054866	<i>ygfB</i>	UPF0149 family protein	3039	3550
b2910	3055612	3055941	<i>zapA</i>	FtsZ stabilizer	892	1686

b2912	3056241	3056789	<i>fau</i>	5-formyltetrahydrofolate cyclo-ligase family protein	393	1277
b2913	3058410	3057178	<i>serA</i>	D-3-phosphoglycerate dehydrogenase	2824	2475
b2914	3059325	3058666	<i>rpiA</i>	ribose 5-phosphate isomerase, constitutive	4577	1745
b2916	3059753	3060646	<i>argP</i>	transcriptional regulator for arginine transport and DNA replication genes; replication initiation inhibitor	724	1479
b2917	3060850	3062994	<i>scpA</i>	methylmalonyl-CoA mutase	115	318
b2918	3062987	3063982	<i>argK</i>	membrane ATPase/protein kinase	23	92
b2919	3063993	3064778	<i>scpB</i>	methylmalonyl-CoA decarboxylase, biotin-independent	48	116
b2920	3064802	3066280	<i>scpC</i>	propionyl-CoA:succinate CoA transferase	98	238
b2921	3067173	3066277	<i>yggI</i>	putative DNA-binding transcriptional regulator	237	324
b2922	3068080	3067340	<i>yggE</i>	oxidative stress defense protein	7306	2188
b2923	3068808	3068173	<i>argO</i>	arginine transporter	74	164
b2924	3069807	3068947	<i>mscS</i>	mechanosensitive channel protein, small conductance	2536	2838
b2925	3071244	3070165	<i>fbaA</i>	fructose-bisphosphate aldolase, class II	58609	9415
b2926	3072622	3071459	<i>pgk</i>	phosphoglycerate kinase	36453	6271
b2927	3073691	3072672	<i>epd</i>	D-erythrose 4-phosphate dehydrogenase	4663	3109
b2928	3074689	3073976	<i>yggC</i>	putative PanK family P-loop kinase	201	451
b2929	3075195	3074686	<i>yggD</i>	MtIR family putative transcriptional repressor	249	464
b2930	3076182	3075217	<i>yggF</i>	fructose 1,6 bisphosphatase isozyme	14	88
b2933	3078859	3077471	<i>cmtA</i>	putative mannitol-specific PTS IIB and IIC components	16	197
b2934	3079330	3078887	<i>cmtB</i>	putative mannitol-specific enzyme IIA component of PTS	19	83
b2935	3081635	3079644	<i>tktA</i>	transketolase 1, thiamine triphosphate-binding	35349	4459
b2936	3081913	3082671	<i>loiP</i>	Phe-Phe periplasmic metalloprotease, OM lipoprotein; low salt-inducible; Era-binding heat shock protein	7532	2306
b2937	3083797	3082877	<i>speB</i>	agmatinase	4503	487
b2938	3085911	3083935	<i>speA</i>	biosynthetic arginine decarboxylase, PLP-binding	17244	3810
b2939	3086051	3085920	<i>yqgB</i>	uncharacterized protein	58	26
b2940	3086187	3086402	<i>yqgC</i>	uncharacterized protein	1569	389
b2942	3086706	3087860	<i>metK</i>	S-adenosylmethionine synthetase	11930	10273
b2943	3088284	3089678	<i>galP</i>	D-galactose transporter	2960	241
b2944	3089755	3090252	<i>yggI</i>	Zn-dependent metalloprotease-related protein	57	91
b2945	3090347	3091054	<i>endA</i>	DNA-specific endonuclease I	77	92
b2946	3091134	3091865	<i>rsmE</i>	16S rRNA m(3)U1498 methyltransferase, SAM-dependent	671	313
b2947	3091878	3092828	<i>gshB</i>	glutathione synthetase	3351	900
b2948	3092937	3093500	<i>yqgE</i>	uncharacterized protein	795	797
b2949	3093500	3093916	<i>yqgF</i>	putative Holliday junction resolvase	406	426
b2950	3095080	3094100	<i>yggR</i>	putative PilT family AAA+ ATPase	22	81
b2951	3095098	3095802	<i>yggS</i>	UPF0001 family protein, PLP-binding	495	300
b2952	3095820	3096386	<i>yggT</i>	putative inner membrane protein; compensates for loss in K ⁺ uptake	816	668
b2953	3096383	3096673	<i>yggU</i>	UPF0235 family protein	231	198
b2954	3096681	3097274	<i>rdgB</i>	dITP/XTP pyrophosphatase	610	205
b2955	3097267	3098403	<i>yggW</i>	HemN family putative oxidoreductase	481	402
b2956	3099565	3098558	<i>yggM</i>	DUF1202 family putative secreted protein	105	731
b2957	3100728	3099682	<i>ansB</i>	periplasmic L-asparaginase 2	34378	2313
b2958	3101623	3100904	<i>yggN</i>	DUF2884 family putative periplasmic protein	683	1324
b2959	3102133	3101807	<i>yggL</i>	DUF469 family protein	2436	1618
b2960	3102852	3102133	<i>trmI</i>	tRNA m(7)G46 methyltransferase, SAM-dependent	1157	1499
b2961	3103013	3104065	<i>mutY</i>	adenine DNA glycosylase	755	472
b2962	3104093	3104368	<i>yggX</i>	oxidative damage protective factor for iron-sulfur proteins	1937	433
b2963	3104433	3105512	<i>mltC</i>	membrane-bound lytic murein transglycosylase C	589	737
b2964	3105714	3106970	<i>nupG</i>	nucleoside transporter	34411	2949
b2965	3109155	3107020	<i>speC</i>	ornithine decarboxylase, constitutive	1832	1796

b2966	3109553	3110260	<i>yggA</i>	DUF554 family putative inner membrane protein	1153	682
b2968	3111126	3110590	<i>yghD</i>	putative membrane-anchored secretion pathway M-type protein	26	149
b2971	3113477	3113067	<i>yghG</i>	secretin (GspDbeta) OM localization lipoprotein pilotin	6	18
b2972	3114352	3113543	<i>pppA</i>	bifunctional prepilin leader peptidase/ methylase	30	132
b2975	3121279	3119597	<i>glcA</i>	glycolate transporter	181	1439
b2976	3123805	3121634	<i>glcB</i>	malate synthase G	4613	9625
b2977	3124231	3123827	<i>glcG</i>	DUF336 family protein	1358	3044
b2979	3128021	3126522	<i>glcD</i>	glycolate oxidase subunit, FAD-linked	854	3688
b2980	3128272	3129036	<i>glcC</i>	glycolate-inducible glc operon transcriptional repressor; autorepressor	4123	458
b2982	3130178	3131194	<i>insHI</i>	IS5 transposase and trans-activator	3143	2558
b2983	3132408	3131341	<i>yghQ</i>	putative inner membrane polysaccharide flippase	66	181
b2984	3133212	3132454	<i>yghR</i>	putative ATP-binding protein	13	60
b2985	3133957	3133244	<i>yghS</i>	putative ATP-binding protein	6	56
b2986	3134131	3134823	<i>yghT</i>	putative ATP-binding protein	4	108
b2987	3136371	3134872	<i>pitB</i>	phosphate transporter	57	93
b2988	3138522	3136663	<i>gss</i>	glutathionylspermidine amidase and glutathionylspermidine synthetase	5785	1861
b2989	3138727	3139593	<i>yghU</i>	putative S-transferase	1779	579
b2990	3139964	3139716	<i>hybG</i>	hydrogenase 2 accessory protein	69	50
b2991	3140318	3139977	<i>hybF</i>	protein involved with the maturation of hydrogenases 1 and 2	37	24
b2992	3140799	3140311	<i>hybE</i>	hydrogenase 2-specific chaperone	253	143
b2993	3141286	3140792	<i>hybD</i>	maturation protease for hydrogenase 2	508	167
b2994	3142989	3141286	<i>hybC</i>	hydrogenase 2, large subunit	2687	548
b2995	3144164	3142986	<i>hybB</i>	putative hydrogenase 2 cytochrome b type component	1029	152
b2996	3145140	3144154	<i>hybA</i>	hydrogenase 2 4Fe-4S ferredoxin-type component	2758	254
b2997	3146261	3145143	<i>hybO</i>	hydrogenase 2, small subunit	5074	644
b2998	3146737	3146450	<i>yghW</i>	DUF2623 family protein	8	64
b3001	3147897	3148937	<i>gpr</i>	L-glyceraldehyde 3-phosphate reductase	12246	1170
b3002	3149471	3148977	<i>yqhA</i>	UPF0114 family putative inner membrane protein	3231	1487
b3003	3149662	3150546	<i>yghA</i>	putative oxidoreductase	246	449
b3005	3151243	3150818	<i>exbD</i>	membrane spanning protein in TonB-ExbB-ExbD complex	3024	1130
b3006	3151984	3151250	<i>exbB</i>	membrane spanning protein in TonB-ExbB-ExbD complex	8264	1759
b3008	3152236	3153423	<i>metC</i>	cystathionine beta-lyase, PLP-dependent	3601	2485
b3009	3153563	3154222	<i>yghB</i>	general envelope maintenance protein; DedA family inner membrane protein; putative multidrug efflux transporter	1824	2488
b3010	3155218	3154262	<i>yqhC</i>	transcriptional activator of yqhD	287	707
b3011	3155355	3156518	<i>yqhD</i>	aldehyde reductase, NADPH-dependent	2930	597
b3012	3156623	3157450	<i>dkgA</i>	2,5-diketo-D-gluconate reductase A	2827	2938
b3013	3157650	3158576	<i>yqhG</i>	DUF3828 family putative periplasmic protein	87	415
b3014	3158627	3158884	<i>yqhH</i>	outer membrane lipoprotein, Lpp paralog	26	53
b3017	3162669	3161257	<i>ftsP</i>	septal ring component that protects the divisome from stress; multicopy suppressor of ftsI(Ts)	1172	621
b3018	3163481	3162744	<i>plsC</i>	1-acyl-sn-glycerol-3-phosphate acyltransferase	734	811
b3019	3165973	3163715	<i>parC</i>	DNA topoisomerase IV, subunit A	2692	1316
b3020	3167718	3166111	<i>ygiS</i>	putative ABC transporter permease	3705	565
b3021	3168246	3167851	<i>mqsA</i>	antitoxin for MqsR toxin; transcriptional repressor	762	2041
b3022	3168544	3168248	<i>mqsR</i>	GCU-specific mRNA interferase toxin of the MqsR-MqsA toxin-antitoxin system; biofilm/motility regulator; anti-repressor	539	6574
b3023	3169231	3168749	<i>ygiV</i>	transcriptional repressor for mcbR biofilm gene	265	101
b3024	3169676	3169284	<i>ygiW</i>	hydrogen peroxide and cadmium resistance periplasmic protein; stress-induced OB-fold protein	3278	683

b3025	3169828	3170487	<i>qseB</i>	quorum sensing DNA-binding response regulator in two-component regulatory system with QseC	323	245
b3026	3170484	3171833	<i>qseC</i>	quorum sensing sensory histidine kinase in two-component regulatory system with QseB	433	271
b3027	3172211	3171879	<i>ygiZ</i>	inner membrane protein	31	556
b3028	3172530	3173111	<i>mdaB</i>	NADPH quinone reductase	799	269
b3029	3173142	3173456	<i>ygiN</i>	quinol monooxygenase	3696	1948
b3030	3175396	3173504	<i>parE</i>	DNA topoisomerase IV, subunit B	3661	1367
b3031	3176006	3175425	<i>yqiA</i>	acyl CoA esterase	1554	342
b3032	3176833	3176006	<i>cpdA</i>	3',5' cAMP phosphodiesterase	5502	1694
b3033	3177280	3176858	<i>yqiB</i>	DUF1249 protein YqiB	415	1553
b3034	3177910	3177281	<i>nudF</i>	ADP-ribose pyrophosphatase	1067	1795
b3035	3178115	3179596	<i>tolC</i>	transport channel	20316	10280
b3037	3179744	3180415	<i>ygiB</i>	DUF1190 family protein	3502	4548
b3038	3180421	3181581	<i>ygiC</i>	ATP-Grasp family ATPase	3157	3397
b3039	3182407	3181619	<i>ygiD</i>	4,5- DOPA-extradiol-dioxygenase	386	406
b3040	3182550	3183323	<i>zupT</i>	zinc transporter	870	945
b3041	3184466	3183813	<i>ribB</i>	3,4-dihydroxy-2-butanone-4-phosphate synthase	4360	2668
b3042	3184840	3185130	<i>yqiC</i>	BMFP family putative fusogenic protein	2313	2080
b3043	3185414	3185965	<i>ygiL</i>	putative fimbrial-like adhesin protein	83	189
b3044	3186187	3186552	<i>insC1</i>	IS2 repressor TnpA	403	429
b3045	3186510	3187415	<i>insD1</i>	IS2 transposase TnpB	652	819
b3047	3189881	3190630	<i>yqiH</i>	putative periplasmic pilin chaperone	45	587
b3048	3190632	3191696	<i>yqiI</i>	fimbrial protein	111	1554
b3049	3191939	3191739	<i>glgS</i>	motility and biofilm regulator	4202	16485
b3050	3192208	3192837	<i>yqiJ</i>	DUF1449 family inner membrane protein	1380	5128
b3051	3192864	3194525	<i>yqiK</i>	PHB family membrane protein, function unknown	1094	1756
b3052	3196753	3195320	<i>hldE</i>	heptose 7-phosphate kinase and heptose 1-phosphate adenylyltransferase	2203	669
b3053	3199641	3196801	<i>glnE</i>	fused deadenylyltransferase/adenylyltransferase for glutamine synthetase	1245	876
b3054	3200965	3199664	<i>ygiF</i>	inorganic triphosphatase	586	477
b3055	3201207	3201827	<i>ygiM</i>	SH3 domain protein	1249	4033
b3056	3201891	3203129	<i>cca</i>	fused tRNA nucleotidyl transferase/2'3'-cyclic phosphodiesterase/2'nucleotidase and phosphatase	962	1083
b3057	3204131	3203310	<i>bacA</i>	undecaprenyl pyrophosphate phosphatase	533	1139
b3058	3204589	3204221	<i>folB</i>	dihydroneopterin aldolase and dihydroneopterin triphosphate 2'-epimerase	191	164
b3059	3204694	3205311	<i>plsY</i>	putative glycerol-3-phosphate acyltransferase	374	599
b3060	3206256	3205324	<i>ttdR</i>	transcriptional activator of ttdABT	1272	434
b3061	3206463	3207374	<i>ttdA</i>	L-tartrate dehydratase, alpha subunit	16	38
b3062	3207371	3207976	<i>ttdB</i>	L-tartrate dehydratase, beta subunit	11	134
b3063	3208024	3209487	<i>ttdT</i>	L-tartrate/succinate antiporte	31	147
b3064	3210543	3209530	<i>tsaD</i>	tRNA(ANN) t(6)A37 threonylcarbamoyladenine modification protein; glycation binding protein	767	496
b3065	3210781	3210996	<i>rpsU</i>	30S ribosomal subunit protein S21	4313	1646
b3066	3211107	3212852	<i>dnaG</i>	DNA primase	1935	7106
b3067	3213047	3214888	<i>rpoD</i>	RNA polymerase, sigma 70 (sigma D) factor	16431	12361
b3068	3215473	3214967	<i>mug</i>	G/U mismatch-specific DNA glycosylase; xanthine DNA glycosylase	1135	986
b3070	3216491	3215727	<i>yqjH</i>	putative siderophore interacting protein	374	155
b3071	3216779	3217402	<i>yqjI</i>	PadR family putative transcriptional regulator	933	460
b3072	3219076	3217556	<i>aer</i>	fused signal transducer for aerotaxis sensory component/methyl accepting chemotaxis component	1840	599
b3073	3219494	3220873	<i>patA</i>	putrescine:2-oxoglutaric acid aminotransferase, PLP-dependent	404	967
b3074	3221247	3220915	<i>yqjH</i>	putative tRNA binding protein; putative tRNA corner chaperone	103	140

b3075	3221466	3222449	<i>ebgR</i>	transcriptional repressor	2124	1044
b3076	3222633	3225725	<i>ebgA</i>	evolved beta-D-galactosidase, alpha subunit	500	256
b3077	3225722	3226171	<i>ebgC</i>	evolved beta-D-galactosidase, beta subunit; cupin superfamily	97	116
b3078	3226234	3227667	<i>ygjI</i>	putative transporter	83	161
b3079	3227801	3228871	<i>ygjJ</i>	putative periplasmic protein	27	372
b3080	3228888	3231239	<i>ygjK</i>	alpha-glucosidase	98	272
b3081	3231665	3233683	<i>fadH</i>	2,4-dienoyl-CoA reductase, NADH and FMN-linked	7302	2938
b3082	3234144	3233728	<i>higA</i>	antitoxin of the HigB-HigA toxin-antitoxin system	512	400
b3083	3234455	3234141	<i>higB</i>	mRNA interferase toxin of the HigB-HigA toxin-antitoxin system	146	849
b3084	3235875	3234739	<i>rlmG</i>	23S rRNA m(2)G1835 methyltransferase, SAM-dependent	278	218
b3085	3235960	3236463	<i>ygjP</i>	putative metal dependent hydrolase	191	212
b3086	3236540	3237232	<i>ygjQ</i>	DUF218 superfamily protein	18	144
b3087	3237311	3238297	<i>ygjR</i>	putative NAD(P)-dependent dehydrogenase	19885	2840
b3088	3238580	3239545	<i>alx</i>	putative membrane-bound redox modulator	79	224
b3089	3239944	3241188	<i>sstT</i>	sodium:serine/threonine symporter	5994	1230
b3090	3241744	3241193	<i>ygjV</i>	Imp-YgjV family inner membrane protein	132	169
b3091	3243314	3241827	<i>uxaA</i>	altronate hydrolase	400	319
b3092	3244741	3243329	<i>uxaC</i>	uronate isomerase	859	308
b3093	3245224	3246522	<i>exuT</i>	hexuronate transporter	677	358
b3094	3246652	3247428	<i>exuR</i>	hexuronate regulon transcriptional repressor; autorepressor	4203	3200
b3095	3247773	3248435	<i>yqjA</i>	general envelope maintenance protein; DedA family inner membrane protein; putative multidrug efflux transporter	1155	2841
b3096	3248439	3248822	<i>mzrA</i>	modulator of EnvZ/OmpR regulon	419	1779
b3097	3248969	3249337	<i>yqjC</i>	DUF1090 family putative periplasmic protein	3324	2032
b3098	3249375	3249680	<i>yqjD</i>	membrane-anchored ribosome-binding protein	2740	910
b3099	3249683	3250087	<i>yqjE</i>	DUF1469 family inner membrane protein	2279	557
b3100	3250077	3250376	<i>yqjK</i>	uncharacterized protein	1620	439
b3101	3250562	3250954	<i>yqjF</i>	putative quinol oxidase subunit	54	235
b3102	3251024	3252010	<i>yqjG</i>	putative S-transferase	1744	1279
b3103	3252304	3252669	<i>yhaH</i>	DUF805 family inner membrane protein	926	395
b3104	3252911	3253267	<i>yhaI</i>	DUF805 family inner membrane protein	29	654
b3105	3254214	3253318	<i>yhaJ</i>	LysR family putative transcriptional regulator	363	502
b3106	3254319	3255020	<i>yhaK</i>	redox-sensitive bicupin	110	94
b3107	3255043	3255207	<i>yhaL</i>	uncharacterized protein	73	64
b3110	3258010	3256679	<i>yhaO</i>	putative transporter	14104	2627
b3113	3260110	3259721	<i>tdcF</i>	putative reactive intermediate deaminase	2711	262
b3114	3262418	3260124	<i>tdcE</i>	pyruvate formate-lyase 4/2-ketobutyrate formate-lyase	16215	703
b3115	3263660	3262452	<i>tdcD</i>	propionate kinase/acetate kinase C, anaerobic	8702	903
b3116	3265017	3263686	<i>tdcC</i>	L-threonine/L-serine transporter	18198	1353
b3117	3266028	3265039	<i>tdcB</i>	L-threonine dehydratase, catabolic	31061	2262
b3118	3267065	3266127	<i>tdcA</i>	tdc operon transcriptional activator	23081	7410
b3119	3267380	3267598	<i>tdcR</i>	L-threonine dehydratase operon activator protein	4	27
b3120	3267854	3268393	<i>yhaB</i>	uncharacterized protein	64	629
b3121	3268415	3269602	<i>yhaC</i>	pentapeptide repeats-related protein	92	675
b3124	3271770	3270625	<i>garK</i>	glycerate kinase I	2405	345
b3125	3272751	3271867	<i>garR</i>	tartronate semialdehyde reductase	4459	319
b3126	3273557	3272787	<i>garL</i>	alpha-dehydro-beta-deoxy-D-glucarate aldolase	5665	384
b3127	3274907	3273573	<i>garP</i>	putative (D)-galactarate transporter	13100	864
b3128	3275282	3276853	<i>garD</i>	D-galactarate dehydrogenase	33170	810
b3129	3277002	3277337	<i>prlF</i>	antitoxin of the SohA(PrIF)-YhaV toxin-antitoxin system	1203	4315

b3130	3277337	3277801	<i>yhaV</i>	toxin of the SohB(PrfF)-YhaV toxin-antitoxin system	1383	3097
b3131	3278665	3277856	<i>agaR</i>	transcriptional repressor of the aga regulon	820	1120
b3132	3278914	3280194	<i>kbaZ</i>	tagatose 6-phosphate aldolase 1, kbaZ subunit	168	65
b3133	3280217	3280690	<i>agaV</i>	N-acetylgalactosamine-specific enzyme IIB component of PTS	72	33
b3136	3281976	3283130	<i>agaS</i>	tagatose-6-phosphate ketose/aldose isomerase	55	82
b3137	3283143	3284003	<i>kbaY</i>	tagatose 6-phosphate aldolase 1, kbaY subunit	27	87
b3138	3284170	3284646	<i>agaB</i>	N-acetylgalactosamine-specific enzyme IIB component of PTS	13	51
b3139	3284685	3285488	<i>agaC</i>	N-acetylgalactosamine-specific enzyme IIC component of PTS	17	46
b3140	3285478	3286269	<i>agaD</i>	N-acetylgalactosamine-specific enzyme IID component of PTS	41	80
b3141	3286270	3287025	<i>agaI</i>	galactosamine-6-phosphate isomerase	22	99
b3142	3287426	3288010	<i>yraH</i>	putative fimbrial-like adhesin protein	90	229
b3143	3288090	3288785	<i>yraI</i>	putative periplasmic pilin chaperone	6	194
b3144	3288814	3291330	<i>yraJ</i>	putative outer membrane protein	717	2008
b3145	3291341	3292432	<i>yraK</i>	putative fimbrial-like adhesin protein	1148	1476
b3146	3293335	3292475	<i>rsml</i>	16S rRNA C1402 2'-O-ribose methyltransferase, SAM-dependent	1086	1442
b3147	3293400	3295436	<i>lpoA</i>	OM lipoprotein stimulator of MrcA transpeptidase	1795	1486
b3148	3295394	3295789	<i>yraN</i>	UPF0102 family protein	383	450
b3149	3295809	3296399	<i>diaA</i>	DnaA initiator-associating factor for replication initiation	818	970
b3150	3296409	3296984	<i>yraP</i>	outer membrane lipoprotein	1725	913
b3151	3298138	3297098	<i>yraQ</i>	putative inner membrane permease	460	337
b3152	3298846	3298211	<i>yraR</i>	putative nucleoside-diphosphate-sugar epimerase	197	168
b3153	3298974	3299492	<i>yhbO</i>	stress-resistance protein	139	283
b3154	3299915	3299472	<i>yhbP</i>	UPF0306 family protein	75	284
b3155	3299966	3300268	<i>yhbQ</i>	GIY-YIG nuclease superfamily protein	190	229
b3156	3300758	3300255	<i>yhbS</i>	GNAT family putative N-acetyltransferase	5928	1315
b3157	3301276	3300752	<i>yhbT</i>	SCP-2 sterol transfer family protein	8823	3206
b3158	3301485	3302480	<i>yhbU</i>	U32 peptidase family protein	679	157
b3159	3302489	3303367	<i>yhbV</i>	U32 peptidase family protein	368	89
b3160	3303448	3304455	<i>yhbW</i>	putative luciferase-like monooxygenase	1065	502
b3161	3305817	3304573	<i>mtr</i>	tryptophan transporter of high affinity	263	5910
b3162	3307860	3305971	<i>deaD</i>	ATP-dependent RNA helicase	4818	2829
b3163	3308924	3308040	<i>nlpI</i>	lipoprotein involved in osmotic sensitivity and filamentation	15350	25561
b3164	3311168	3309033	<i>pnp</i>	polynucleotide phosphorylase/polyadenylase	28634	12519
b3165	3311684	3311415	<i>rpsO</i>	30S ribosomal subunit protein S15	18707	13168
b3166	3312777	3311833	<i>truB</i>	tRNA pseudouridine synthase B: tRNA pseudouridine(55) synthase and putative tmRNA pseudouridine(342) synthase	2202	972
b3167	3313178	3312777	<i>rbfA</i>	30s ribosome binding factor	1872	478
b3168	3316014	3313342	<i>infB</i>	translation initiation factor IF-2	39835	10205
b3169	3317526	3316039	<i>nusA</i>	transcription termination/antitermination L factor	9562	3672
b3170	3318006	3317554	<i>rimP</i>	ribosome maturation factor for 30S subunits	1160	653
b3172	3318637	3319980	<i>argG</i>	argininosuccinate synthetase	1899	9631
b3173	3321613	3319988	<i>yhbX</i>	putative EptAB family phosphoethanolamine transferase, inner membrane protein	162	758
b3175	3322505	3322173	<i>secG</i>	preprotein translocase membrane subunit	3026	1393
b3176	3324070	3322733	<i>glmM</i>	phosphoglucosamine mutase	9688	1536
b3177	3324911	3324063	<i>folP</i>	7,8-dihydropteroate synthase	1073	338
b3178	3326935	3325001	<i>ftsH</i>	protease, ATP-dependent zinc-metallo	23230	10413
b3179	3327664	3327035	<i>rlmE</i>	23S rRNA U2552 2'-O-ribose methyltransferase, SAM-dependent	6596	9261
b3180	3327790	3328083	<i>yhbY</i>	RNA binding protein associated with pre-50S ribosomal	1383	2010

				subunits		
b3181	3328715	3328239	<i>greA</i>	transcript cleavage factor	978	721
b3182	3328963	3330396	<i>dacB</i>	D-alanyl-D-alanine carboxypeptidase	541	367
b3183	3331754	3330582	<i>obgE</i>	GTPase involved in cell partitioning and DNA repair	2745	1414
b3184	3332735	3331770	<i>yhbE</i>	EamA family inner membrane putative transporter	592	741
b3185	3333119	3332862	<i>rpmA</i>	50S ribosomal subunit protein L27	9953	8623
b3186	3333451	3333140	<i>rplU</i>	50S ribosomal subunit protein L21	5910	4074
b3187	3333710	3334681	<i>ispB</i>	octaprenyl diphosphate synthase	2705	1771
b3188	3334909	3335187	<i>sfsB</i>	malPQ operon transcriptional activator	105	105
b3189	3336494	3335235	<i>murA</i>	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	5283	1456
b3190	3336803	3336549	<i>ibaG</i>	acid stress protein; putative BolA family transcriptional regulator	781	553
b3191	3337256	3336963	<i>mlaB</i>	ABC transporter maintaining OM lipid asymmetry, cytoplasmic STAS component	1377	841
b3192	3337891	3337256	<i>mlaC</i>	ABC transporter maintaining OM lipid asymmetry, periplasmic binding protein	2876	1464
b3193	3338461	3337910	<i>mldD</i>	OM lipid asymmetry maintenance protein; membrane-anchored ABC family periplasmic binding protein	1026	634
b3194	3339248	3338466	<i>mldE</i>	ABC transporter maintaining OM lipid asymmetry, inner membrane permease protein	925	538
b3195	3340065	3339256	<i>mldF</i>	ABC transporter maintaining OM lipid asymmetry, ATP-binding protein	1494	1569
b3196	3340275	3341252	<i>yrbG</i>	putative calcium/sodium:proton antiporter	434	509
b3197	3341266	3342252	<i>kdsD</i>	D-arabinose 5-phosphate isomerase	1444	2039
b3198	3342273	3342839	<i>kdsC</i>	3-deoxy-D-manno-octulosonate 8-phosphate phosphatase	1047	1098
b3199	3342836	3343411	<i>lptC</i>	periplasmic membrane-anchored LPS-binding protein; LPS export protein	2122	2903
b3200	3343380	3343937	<i>lptA</i>	lipopolysaccharide export ABC transporter periplasmic binding protein; Lipid A binding protein; LPS export and assembly protein	3751	2740
b3201	3343944	3344669	<i>lptB</i>	lipopolysaccharide export ABC transporter ATPase	1479	565
b3202	3344717	3346150	<i>rpoN</i>	RNA polymerase, sigma 54 (sigma N) factor	4971	4359
b3203	3346173	3346460	<i>hpf</i>	ribosome hibernation promoting factor HPF; stabilizes 100S dimers	2659	2853
b3204	3346578	3347069	<i>ptsN</i>	sugar-specific enzyme IIA component of PTS	1377	561
b3205	3347115	3347969	<i>yhbJ</i>	adaptor protein for GlmZ/GlmY sRNA decay, glucosamine-6-phosphate-regulated; NTPase	2557	1205
b3206	3347966	3348238	<i>npr</i>	phosphohistidinoprotein-hexose phosphotransferase component of N-regulated PTS system (Npr)	128	190
b3207	3348452	3349084	<i>yrbL</i>	Mg(2+)-starvation-stimulated protein	151	438
b3208	3349809	3349081	<i>mtgA</i>	biosynthetic peptidoglycan transglycosylase	415	422
b3209	3350459	3349806	<i>elbB</i>	isoprenoid biosynthesis protein with amidotransferase-like domain	1024	417
b3210	3353025	3350689	<i>arcB</i>	aerobic respiration control sensor histidine protein kinase, cognate to two-component response regulators ArcA and RssB	4922	3509
b3211	3354050	3353121	<i>yhcC</i>	putative Fe-S oxidoreductase, Radical SAM superfamily protein	138	149
b3212	3354725	3359185	<i>glbB</i>	glutamate synthase, large subunit	2122	2310
b3213	3359198	3360616	<i>glbD</i>	glutamate synthase, 4Fe-4S protein, small subunit	740	641
b3214	3361176	3361940	<i>glbF</i>	periplasmic protein	427	241
b3215	3362112	3362786	<i>yhcA</i>	putative periplasmic chaperone protein	10	177
b3216	3362807	3365188	<i>yhcD</i>	putative outer membrane fimbrial subunit usher protein	257	1709
b3218	3366718	3365702	<i>insH1</i>	IS5 transposase and trans-activator	3143	2558
b3219	3366926	3367642	<i>yhcF</i>	putative transcriptional regulator	387	2581
b3220	3367827	3368954	<i>yhcG</i>	DUF1016 family protein in the PD-(D/E)XK nuclease superfamily	138	225
b3221	3369478	3369014	<i>yhcH</i>	DUF386 family protein, cupin superfamily	663	280
b3222	3370350	3369475	<i>nanK</i>	N-acetylmannosamine kinase	825	80
b3223	3371036	3370347	<i>nanE</i>	putative N-acetylmannosamine-6-P epimerase	827	41

b3224	3372574	3371084	<i>nanT</i>	sialic acid transporter	2899	164
b3225	3373576	3372683	<i>nanA</i>	N-acetylneuraminate lyase	15575	287
b3226	3374489	3373698	<i>nanR</i>	sialic acid-inducible nan operon repressor	1463	1186
b3227	3374869	3376236	<i>dcuD</i>	putative transporter	103	549
b3228	3376776	3376279	<i>sspB</i>	ClpXP protease specificity enhancing factor	1607	452
b3229	3377420	3376782	<i>sspA</i>	stringent starvation protein A, phage P1 late gene activator, RNAP-associated acid-resistance protein, inactive glutathione S-transferase homolog	4733	1229
b3230	3378207	3377815	<i>rpsI</i>	30S ribosomal subunit protein S9	11986	4962
b3231	3378651	3378223	<i>rplM</i>	50S ribosomal subunit protein L13	8641	6286
b3232	3379997	3378870	<i>zapE</i>	divisome ATPase	557	906
b3233	3380191	3380589	<i>yhcB</i>	DUF1043 family inner membrane-anchored protein	3726	1941
b3234	3380743	3382110	<i>degQ</i>	serine endoprotease, periplasmic	2554	1722
b3235	3382200	3383267	<i>degS</i>	serine endoprotease, periplasmic	620	763
b3236	3384268	3383330	<i>mdh</i>	malate dehydrogenase, NAD(P)-binding	98433	18170
b3237	3384703	3385173	<i>argR</i>	l-arginine-responsive arginine metabolism regulon transcriptional regulator	1240	2345
b3238	3385538	3385801	<i>yhcN</i>	cadmium and peroxide resistance protein, stress-induced	532	1325
b3239	3386129	3385857	<i>yhcO</i>	putative barnase inhibitor	233	319
b3240	3388188	3386221	<i>aaeB</i>	p-hydroxybenzoic acid efflux system component	68	294
b3241	3389126	3388194	<i>aaeA</i>	p-hydroxybenzoic acid efflux system component	109	811
b3242	3389337	3389134	<i>aaeX</i>	DUF1656 family putative inner membrane efflux pump associated protein	43	198
b3243	3389520	3390449	<i>aaeR</i>	transcriptional regulator for aaeXAB operon	699	1044
b3244	3392028	3390583	<i>tldD</i>	putative peptidase	4496	2089
b3247	3397795	3396326	<i>rng</i>	ribonuclease G	2374	2002
b3248	3398378	3397785	<i>yhdE</i>	dTTP/UTP pyrophosphatase; m(5)UTP/m(5)CTP/pseudo-UTP pyrophosphatase	844	1075
b3249	3398875	3398387	<i>mreD</i>	cell wall structural complex MreBCD transmembrane component MreD	264	387
b3250	3399978	3398875	<i>mreC</i>	cell wall structural complex MreBCD transmembrane component MreC	798	591
b3251	3401087	3400044	<i>mreB</i>	cell wall structural complex MreBCD, actin-like component MreB	5496	2414
b3252	3403332	3401392	<i>csrD</i>	targeting factor for csrBC sRNA degradation	1201	2040
b3253	3403484	3404458	<i>acul</i>	putative acryloyl-CoA reductase	2587	603
b3255	3405436	3405906	<i>accB</i>	acetyl CoA carboxylase, BCCP subunit	7560	1652
b3256	3405917	3407266	<i>accC</i>	acetyl-CoA carboxylase, biotin carboxylase subunit	15903	2493
b3257	3407375	3407617	<i>yhdT</i>	DUF997 family putative inner membrane protein	33	55
b3258	3407607	3409058	<i>panF</i>	pantothenate:sodium symporter	242	311
b3259	3409070	3409951	<i>prmA</i>	methyltransferase for 50S ribosomal subunit protein L11	978	368
b3260	3410280	3411245	<i>dusB</i>	tRNA-dihydrouridine synthase B	1483	3023
b3261	3411271	3411567	<i>fis</i>	global DNA-binding transcriptional dual regulator	1432	5017
b3262	3411653	3412537	<i>yhdJ</i>	DNA adenine methyltransferase, SAM-dependent	64	446
b3263	3412621	3412800	<i>yhdU</i>	putative membrane protein	53	826
b3264	3413465	3412803	<i>acrS</i>	acrAB operon transcriptional repressor	23	1915
b3265	3413864	3415021	<i>acrE</i>	cytoplasmic membrane lipoprotein	25	107
b3266	3415033	3418137	<i>acrF</i>	multidrug efflux system protein	159	627
b3267	3418390	3418611	<i>yhdV</i>	putative outer membrane protein	53	225
b3269	3420134	3421315	<i>yhdX</i>	putative amino acid ABC transporter permease	68	389
b3270	3421325	3422428	<i>yhdY</i>	putative amino acid ABC transporter permease	39	160
b3271	3422436	3423194	<i>yhdZ</i>	putative amino acid ABC transporter ATPase	136	453
b3279	3429236	3429790	<i>yrdA</i>	bacterial transferase hexapeptide domain protein	2706	3026
b3280	3430023	3429766	<i>yrdB</i>	DUF1488 family protein	581	483
b3281	3430838	3430020	<i>aroE</i>	dehydroshikimate reductase, NAD(P)-binding	1151	609
b3282	3431415	3430843	<i>tsaC</i>	tRNA(ANN) t(6)A37 threonylcarbamoyladenosine modification protein, threonine-dependent ADP-forming	873	577

				ATPase		
b3283	3431962	3431420	<i>yrdD</i>	ssDNA-binding protein, function unknown	1636	4129
b3284	3432464	3431991	<i>smg</i>	DUF494 family putative periplasmic protein	2270	2600
b3287	3433690	3434199	<i>def</i>	peptide deformylase	4684	8637
b3288	3434214	3435161	<i>fnt</i>	10-formyltetrahydrofolate:L-methionyl-tRNA(fMet) N-formyltransferase	3970	2214
b3289	3435207	3436496	<i>rsmB</i>	16S rRNA m(5)C967 methyltransferase, SAM-dependent	1573	851
b3290	3436518	3437894	<i>trkA</i>	NAD-binding component of TrK potassium transporter	2049	1497
b3291	3438024	3438434	<i>mscL</i>	mechanosensitive channel protein, high conductance	3565	3240
b3292	3439130	3438705	<i>zntR</i>	zntA gene transcriptional activator	841	991
b3293	3439509	3439141	<i>yhdN</i>	DUF1992 family protein	683	1413
b3294	3439999	3439616	<i>rplQ</i>	50S ribosomal subunit protein L17	22402	4398
b3295	3441029	3440040	<i>rpoA</i>	RNA polymerase, alpha subunit	78128	17257
b3296	3441675	3441055	<i>rpsD</i>	30S ribosomal subunit protein S4	44089	9204
b3297	3442098	3441709	<i>rpsK</i>	30S ribosomal subunit protein S11	19048	3805
b3298	3442471	3442115	<i>rpsM</i>	30S ribosomal subunit protein S13	17023	4221
b3299	3442734	3442618	<i>rpmJ</i>	50S ribosomal subunit protein L36	2945	1781
b3300	3444097	3442766	<i>secY</i>	preprotein translocase membrane subunit	83889	22752
b3301	3444539	3444105	<i>rplO</i>	50S ribosomal subunit protein L15	49974	6625
b3302	3444722	3444543	<i>rpmD</i>	50S ribosomal subunit protein L30	14103	2500
b3303	3445229	3444726	<i>rpsE</i>	30S ribosomal subunit protein S5	45252	8585
b3304	3445597	3445244	<i>rplR</i>	50S ribosomal subunit protein L18	23102	3501
b3305	3446140	3445607	<i>rplF</i>	50S ribosomal subunit protein L6	42787	6826
b3306	3446545	3446153	<i>rpsH</i>	30S ribosomal subunit protein S8	23032	9778
b3307	3446884	3446579	<i>rpsN</i>	30S ribosomal subunit protein S14	27178	5815
b3308	3447438	3446899	<i>rplE</i>	50S ribosomal subunit protein L5	43547	9595
b3309	3447767	3447453	<i>rplX</i>	50S ribosomal subunit protein L24	22551	5433
b3310	3448149	3447778	<i>rplN</i>	50S ribosomal subunit protein L14	40846	16457
b3311	3448568	3448314	<i>rpsQ</i>	30S ribosomal subunit protein S17	74492	17571
b3312	3448759	3448568	<i>rpmC</i>	50S ribosomal subunit protein L29	30159	4910
b3313	3449169	3448759	<i>rplP</i>	50S ribosomal subunit protein L16	56243	7928
b3314	3449883	3449182	<i>rpsC</i>	30S ribosomal subunit protein S3	80769	10324
b3315	3450233	3449901	<i>rplV</i>	50S ribosomal subunit protein L22	35631	6879
b3316	3450526	3450248	<i>rpsS</i>	30S ribosomal subunit protein S19	21515	8066
b3317	3451364	3450543	<i>rplB</i>	50S ribosomal subunit protein L2	60130	8719
b3318	3451684	3451382	<i>rplW</i>	50S ribosomal subunit protein L23	25844	5784
b3319	3452286	3451681	<i>rplD</i>	50S ribosomal subunit protein L4	33308	4761
b3320	3452926	3452297	<i>rplC</i>	50S ribosomal subunit protein L3	52502	8493
b3321	3453270	3452959	<i>rpsJ</i>	30S ribosomal subunit protein S10	22752	4349
b3322	3453927	3453508	<i>gspB</i>	part of gsp divergon involved in type II protein secretion	75	209
b3323	3455398	3453929	<i>gspA</i>	general secretory pathway component, cryptic	42	520
b3324	3455578	3456393	<i>gspC</i>	general secretory pathway component, cryptic	41	279
b3325	3456377	3458329	<i>gspD</i>	general secretory pathway component, cryptic	158	525
b3326	3458339	3459820	<i>gspE</i>	general secretory pathway component, cryptic	60	124
b3327	3459817	3461013	<i>gspF</i>	general secretory pathway component, cryptic	106	384
b3328	3461023	3461460	<i>gspG</i>	pseudopilin, cryptic, general secretion pathway	23	40
b3329	3461468	3461977	<i>gspH</i>	putative general secretory pathway component, cryptic	10	22
b3330	3461974	3462351	<i>gspI</i>	general secretory pathway component, cryptic	10	61
b3331	3462344	3462931	<i>gspJ</i>	putative general secretory pathway component, cryptic	30	123
b3332	3462924	3463907	<i>gspK</i>	general secretory pathway component, cryptic	142	210
b3333	3463922	3465085	<i>gspL</i>	general secretory pathway component, cryptic	188	804
b3334	3465082	3465543	<i>gspM</i>	general secretory pathway component, cryptic	63	327
b3335	3465543	3466220	<i>gspO</i>	bifunctional prepilin leader peptidase/ methylase	214	1446

b3336	3466725	3466249	<i>bfr</i>	bacterioferritin, iron storage and detoxification protein	10625	11219
b3337	3466991	3466797	<i>bfd</i>	bacterioferritin-associated ferredoxin	1036	1525
b3338	3469853	3467160	<i>chiA</i>	periplasmic endochitinase	758	877
b3339	3471329	3470145	<i>tufA</i>	translation elongation factor EF-Tu 1	269905	40898
b3340	3473514	3471400	<i>fusA</i>	protein chain elongation factor EF-G, GTP-binding	246222	56385
b3341	3474081	3473542	<i>rpsG</i>	30S ribosomal subunit protein S7	38913	8701
b3342	3474552	3474178	<i>rpsL</i>	30S ribosomal subunit protein S12	31100	4457
b3343	3474965	3474678	<i>tusB</i>	mm(5)-s(2)U34-tRNA synthesis 2-thiolation protein	293	615
b3344	3475332	3474973	<i>tusC</i>	mm(5)-s(2)U34-tRNA synthesis 2-thiolation protein	155	132
b3345	3475718	3475332	<i>tusD</i>	sulfurtransferase for 2-thiolation step of mm(5)-s(2)U34-tRNA synthesis	521	422
b3346	3476440	3475718	<i>yheO</i>	putative PAS domain-containing DNA-binding transcriptional regulator	2004	1677
b3347	3477419	3476607	<i>fkpA</i>	FKBP-type peptidyl-prolyl cis-trans isomerase (rotamase)	14257	10430
b3348	3477640	3477858	<i>slyX</i>	phi X174 lysis protein	531	741
b3349	3478497	3477907	<i>slyD</i>	FKBP-type peptidyl prolyl cis-trans isomerase (rotamase)	10550	3236
b3350	3480607	3478802	<i>kefB</i>	potassium:proton antiporter	1092	1003
b3351	3481161	3480607	<i>kefG</i>	potassium-efflux system ancillary protein for KefB, glutathione-regulated	403	410
b3352	3481289	3483202	<i>yheS</i>	ABC-F family protein predicted regulatory ATPase	1178	985
b3353	3483202	3484224	<i>yheT</i>	UPF0017 family putative hydrolase	343	212
b3354	3484218	3484436	<i>yheU</i>	UPF0270 family protein	146	139
b3355	3484490	3485359	<i>prkB</i>	putative phosphoribulokinase	886	1513
b3356	3485818	3485414	<i>yhfA</i>	OsmC family protein	2534	915
b3357	3486120	3486752	<i>crp</i>	cAMP-activated global transcription factor, mediator of catabolite repression	34616	19699
b3358	3486791	3488893	<i>yhfK</i>	putative transporter, FUSC superfamily inner membrane protein	750	1145
b3359	3490180	3488960	<i>argD</i>	bifunctional acetylornithine aminotransferase and succinyldiaminopimelate aminotransferase	331	2678
b3360	3490829	3490266	<i>pabA</i>	aminodeoxychorismate synthase, subunit II	213	149
b3361	3491463	3490861	<i>fic</i>	stationary phase-induced protein, putative toxin	1665	958
b3362	3491620	3491453	<i>yhfG</i>	putative antitoxin for Fic	152	160
b3363	3492297	3491725	<i>ppiA</i>	peptidyl-prolyl cis-trans isomerase A (rotamase A)	1347	1152
b3364	3492568	3493749	<i>tsgA</i>	putative transporter	216	429
b3365	3494011	3496554	<i>nirB</i>	nitrite reductase, large subunit, NAD(P)H-binding	11799	1041
b3366	3496551	3496877	<i>nirD</i>	nitrite reductase (NADH) small subunit	574	26
b3367	3497003	3497809	<i>nirC</i>	nitrite transporter	368	92
b3368	3497828	3499201	<i>cysG</i>	fused siroheme synthase 1,3-dimethyluroporphyriongen III dehydrogenase and siroheme ferrochelatase/uroporphyrinogen methyltransferase	1008	772
b3369	3499448	3499615	<i>yhfL</i>	small lipoprotein	65	88
b3370	3499910	3501247	<i>frlA</i>	putative fructoselysine transporter	81	90
b3371	3501268	3502290	<i>frlB</i>	fructoselysine-6-P-deglycase	106	65
b3374	3503167	3503952	<i>frlD</i>	fructoselysine 6-kinase	63	65
b3375	3504052	3504783	<i>frlR</i>	putative DNA-binding transcriptional regulator	487	514
b3376	3506020	3504935	<i>yhfS</i>	FNR-regulated pyridoxal phosphate-dependent aminotransferase family protein	49	119
b3377	3507336	3506032	<i>yhfT</i>	inner membrane protein	84	161
b3378	3507701	3507348	<i>yhfU</i>	DUF2620 family protein	34	75
b3379	3508590	3507712	<i>php</i>	phosphotriesterase homology protein	69	211
b3380	3509813	3508587	<i>yhfW</i>	phosphopentomutase-related metalloenzyme superfamily protein	70	157
b3381	3510976	3509813	<i>yhfX</i>	putative pyridoxal 5'-phosphate binding protein	75	57
b3382	3511422	3511060	<i>yhfY</i>	PRD domain protein	247	93
b3383	3512344	3511439	<i>yhfZ</i>	putative DNA-binding transcriptional regulator	672	688
b3384	3513638	3512634	<i>trpS</i>	tryptophanyl-tRNA synthetase	5443	1566

b3385	3514389	3513631	<i>gph</i>	phosphoglycolate phosphatase	1619	541
b3386	3515059	3514382	<i>rpe</i>	D-ribulose-5-phosphate 3-epimerase	1886	517
b3387	3515913	3515077	<i>dam</i>	DNA adenine methyltransferase	827	654
b3388	3517306	3516020	<i>damX</i>	cell division protein that binds to the septal ring	10168	5251
b3389	3518486	3517398	<i>aroB</i>	3-dehydroquinate synthase	4500	3291
b3390	3519064	3518543	<i>aroK</i>	shikimate kinase I	3058	2543
b3391	3520703	3519465	<i>hofQ</i>	DNA catabolic putative fimbrial transporter	116	203
b3392	3521019	3520615	<i>hofP</i>	DNA catabolic protein	30	131
b3393	3521449	3521009	<i>hofO</i>	DNA catabolic protein	18	24
b3394	3521972	3521433	<i>hofN</i>	DNA catabolic putative fimbrial assembly protein	25	19
b3395	3522751	3521972	<i>hofM</i>	DNA catabolic putative pilus assembly protein	127	119
b3396	3522871	3525423	<i>mrcA</i>	penicillin-binding protein 1a, murein transglycosylase and transpeptidase	1027	1095
b3397	3526149	3525589	<i>nudE</i>	adenosine nucleotide hydrolase; Ap3A/Ap2A/ADP-ribose/NADH hydrolase	852	947
b3398	3526469	3528604	<i>yrfF</i>	putative RcsCDB-response attenuator, inner membrane protein	1112	1141
b3399	3528669	3529337	<i>yrfG</i>	GMP/IMP nucleotidase	1476	1169
b3400	3529348	3529749	<i>hslR</i>	ribosome-associated heat shock protein Hsp15	1224	709
b3401	3529774	3530652	<i>hslO</i>	heat shock protein Hsp33	4777	1765
b3402	3532439	3530715	<i>yhgE</i>	DUF4153 family putative inner membrane protein	678	1350
b3403	3532818	3534440	<i>pck</i>	phosphoenolpyruvate carboxykinase [ATP]	87458	8063
b3404	3535868	3534516	<i>envZ</i>	sensory histidine kinase in two-component regulatory system with OmpR	1115	495
b3405	3536584	3535865	<i>ompR</i>	response regulator in two-component regulatory system with EnvZ	4796	1467
b3406	3536812	3537288	<i>greB</i>	transcript cleavage factor	466	374
b3407	3537385	3539706	<i>yhgF</i>	putative transcriptional accessory protein	2138	762
b3408	3540163	3540390	<i>feoA</i>	ferrous iron transporter, protein A	2495	427
b3409	3540407	3542728	<i>feoB</i>	ferrous iron transporter protein B and GTP-binding protein; membrane protein	20259	2120
b3410	3542728	3542964	<i>feoC</i>	putative DNA-binding transcriptional regulator	529	133
b3411	3543167	3544045	<i>yhgA</i>	transposase_31 family protein	201	593
b3412	3544844	3544074	<i>bioH</i>	pimeloyl-ACP methyl ester carboxylesterase	295	179
b3413	3544882	3545565	<i>gntX</i>	DNA catabolic protein	330	509
b3414	3545624	3546199	<i>nfuA</i>	Fe/S biogenesis protein, putative scaffold/chaperone protein	4735	3044
b3415	3546559	3547875	<i>gntT</i>	gluconate transporter, high-affinity GNT I system	1345	702
b3416	3550070	3547986	<i>malQ</i>	4-alpha-glucanotransferase (amylomaltase)	25291	3756
b3417	3552473	3550080	<i>malP</i>	maltodextrin phosphorylase	22425	3680
b3418	3553085	3555790	<i>malT</i>	mal regulon transcriptional activator	30607	14592
b3421	3558079	3556853	<i>rtcB</i>	RNA-splicing ligase	144	303
b3422	3558268	3559866	<i>rtcR</i>	sigma 54-dependent transcriptional regulator of rtcBA expression	92	130
b3424	3561452	3560622	<i>glpG</i>	rhomboid intramembrane serine protease	357	515
b3425	3561823	3561497	<i>glpE</i>	thiosulfate:cyanide sulfurtransferase (rhodanese)	98	661
b3426	3562013	3563518	<i>glpD</i>	sn-glycerol-3-phosphate dehydrogenase, aerobic, FAD/NAD(P)-binding	2819	9425
b3428	3566581	3564134	<i>glgP</i>	glycogen phosphorylase	7555	2861
b3429	3568033	3566600	<i>glgA</i>	glycogen synthase	3043	1122
b3430	3569328	3568033	<i>glgC</i>	glucose-1-phosphate adenyltransferase	8133	2781
b3431	3571319	3569346	<i>glgX</i>	glycogen debranching enzyme	3080	2524
b3432	3573502	3571316	<i>glgB</i>	1,4-alpha-glucan branching enzyme	3282	2833
b3433	3574878	3573775	<i>asd</i>	aspartate-semialdehyde dehydrogenase, NAD(P)-binding	6032	3649
b3434	3575071	3575664	<i>yhgN</i>	UPF0056 family inner membrane protein	279	172
b3437	3577592	3577065	<i>gntK</i>	gluconate kinase 2	726	176
b3438	3578726	3577731	<i>gntR</i>	d-gluconate inducible gluconate regulon transcriptional	2422	1281

				repressor		
b3439	3579645	3578950	<i>yhhW</i>	quercetinase activity in vitro	716	386
b3440	3580805	3579768	<i>yhhX</i>	putative oxidoreductase	2930	1669
b3441	3581138	3581626	<i>yhhY</i>	aminoacyl nucleotide detoxifying acetyltransferase	180	186
b3442	3581863	3583041	<i>yhhZ</i>	putative Hcp1 family polymorphic toxin protein; putative colicin-like DNase/tRNase activity	11	1566
b3444	3583483	3583758	<i>insA</i>	IS1 repressor TnpA	96	513
b3445	3583677	3584180	<i>insB1</i>	IS1 transposase B	721	1067
b3446	3584759	3585043	<i>yrhB</i>	stable heat shock chaperone	16	149
b3447	3586823	3585081	<i>ggt</i>	gamma-glutamyltranspeptidase	293	270
b3448	3586943	3587383	<i>yhhA</i>	DUF2756 family protein	4176	4167
b3449	3588113	3587370	<i>ugpQ</i>	glycerophosphodiester phosphodiesterase, cytosolic	696	324
b3450	3589180	3588110	<i>ugpC</i>	sn-glycerol-3-phosphate ABC transporter ATPase	880	295
b3451	3590027	3589182	<i>ugpE</i>	sn-glycerol-3-phosphate ABC transporter permease	241	127
b3452	3590911	3590024	<i>ugpA</i>	sn-glycerol-3-phosphate ABC transporter permease	179	211
b3453	3592325	3591009	<i>ugpB</i>	sn-glycerol-3-phosphate ABC transporter periplasmic binding protein	9461	5874
b3454	3593437	3592724	<i>livF</i>	branched-chain amino acid ABC transporter ATPase	237	246
b3455	3594206	3593439	<i>livG</i>	branched-chain amino acid ABC transporter ATPase	99	139
b3456	3595480	3594203	<i>livM</i>	branched-chain amino acid ABC transporter permease	82	150
b3457	3596403	3595477	<i>livH</i>	branched-chain amino acid ABC transporter permease	42	87
b3458	3597560	3596451	<i>livK</i>	leucine transporter subunit	219	918
b3459	3597984	3598367	<i>panM</i>	PanD autocleavage accelerator, pantothenate synthesis	245	154
b3460	3599658	3598555	<i>livJ</i>	branched-chain amino acid ABC transporter periplasmic binding protein	433	2638
b3461	3600783	3599929	<i>rpoH</i>	RNA polymerase, sigma 32 (sigma H) factor	5984	4622
b3462	3602086	3601028	<i>ftsX</i>	putative ABC transporter permease	1445	654
b3463	3602747	3602079	<i>ftsE</i>	cell division ATP-binding protein	903	275
b3464	3604243	3602750	<i>ftsY</i>	Signal Recognition Particle (SRP) receptor	2589	1836
b3465	3604393	3604989	<i>rsmD</i>	16S rRNA m(2)G966 methyltransferase, SAM-dependent	516	456
b3466	3604979	3605248	<i>yhhL</i>	DUF1145 family protein	158	149
b3467	3605610	3605251	<i>yhhM</i>	DUF2500 family protein	358	435
b3468	3605751	3606377	<i>yhhN</i>	TMEM86 family putative inner membrane protein	737	335
b3469	3606451	3608649	<i>zntA</i>	zinc, cobalt and lead efflux system	1515	1345
b3470	3608996	3608751	<i>tusA</i>	mm(5)-s(2)U34-tRNA 2-thiolation sulfurtransferase	127	505
b3471	3609217	3609882	<i>yhhQ</i>	DUF165 family inner membrane protein	160	1114
b3472	3609955	3610512	<i>dcrB</i>	putative lipoprotein	13990	4061
b3473	3611733	3610516	<i>yhhS</i>	putative arabinose efflux transporter	199	197
b3474	3611865	3612914	<i>yhhT</i>	UPF0118 family putative transporter	501	331
b3475	3612969	3613556	<i>acpT</i>	4'-phosphopantetheinyl transferase	230	258
b3476	3613667	3615241	<i>nikA</i>	nickel/heme ABC transporter periplasmic binding protein	3848	362
b3477	3615241	3616185	<i>nikB</i>	nickel ABC transporter permease	416	83
b3478	3616182	3617015	<i>nikC</i>	nickel ABC transporter permease	212	34
b3479	3617015	3617779	<i>nikD</i>	nickel ABC transporter ATPase	411	103
b3480	3617776	3618582	<i>nikE</i>	nickel ABC transporter ATPase	376	78
b3481	3618588	3618989	<i>nikR</i>	transcriptional repressor, Ni-binding	360	221
b3482	3619192	3623427	<i>rhsB</i>	Rhs protein with DUF4329 family putative toxin domain; putative neighboring cell growth inhibitor	373	1179
b3483	3623399	3623782	<i>yhhH</i>	putative NTF2 fold immunity protein for polymorphic toxin RhsB	23	968
b3484	3624378	3625514	<i>yhhI</i>	putative transposase	75	2233
b3485	3626803	3625679	<i>yhhJ</i>	putative ABC transporter permease	124	431
b3486	3629538	3626803	<i>rbbA</i>	ribosome-associated ATPase: ATP-binding protein/ATP-binding membrane protein	411	679
b3487	3630602	3629535	<i>yhiI</i>	putative membrane fusion protein (MFP) of efflux pump	528	925

b3488	3632590	3630968	<i>yhiJ</i>	DUF4049 family protein	45	960
b3491	3634841	3635893	<i>yhiM</i>	acid resistance protein, inner membrane	0	0
b3492	3637410	3636208	<i>yhiN</i>	putative oxidoreductase	0	1
b3493	3637642	3639141	<i>pitA</i>	phosphate transporter, low-affinity; tellurite importer	43	142
b3494	3639720	3639385	<i>uspB</i>	universal stress (ethanol tolerance) protein B	745	588
b3495	3640111	3640545	<i>uspA</i>	universal stress global response regulator	24794	26565
b3496	3640862	3642331	<i>dtpB</i>	dipeptide and tripeptide permease B	11543	985
b3497	3643132	3642380	<i>rsmJ</i>	16S rRNA m(2)G1516 methyltransferase, SAM-dependent	342	156
b3498	3645182	3643140	<i>prlC</i>	oligopeptidase A	4328	2578
b3499	3645385	3646227	<i>rlmJ</i>	23S rRNA m(6)A2030 methyltransferase, SAM-dependent	609	716
b3500	3646299	3647651	<i>gor</i>	glutathione oxidoreductase	2886	2041
b3501	3648528	3648881	<i>arsR</i>	arsenical resistance operon transcriptional repressor; autorepressor	29	151
b3502	3648935	3650224	<i>arsB</i>	arsenite/antimonite transporter	66	326
b3503	3650237	3650662	<i>arsC</i>	arsenate reductase	66	70
b3505	3653198	3652182	<i>insH1</i>	IS5 transposase and trans-activator	3143	2558
b3506	3653961	3654527	<i>slp</i>	outer membrane lipoprotein	0	0
b3509	3656292	3655966	<i>hdeB</i>	acid-resistance protein	0	2
b3510	3656740	3656408	<i>hdeA</i>	stress response protein acid-resistance protein	0	1
b3511	3656995	3657567	<i>hdeD</i>	acid-resistance membrane protein	0	1
b3512	3658366	3658893	<i>gadE</i>	gad regulon transcriptional activator	0	2
b3513	3659232	3660389	<i>mdtE</i>	anaerobic multidrug efflux transporter, ArcA-regulated	0	1
b3514	3660414	3663527	<i>mdtF</i>	anaerobic multidrug efflux transporter, ArcA-regulated	0	1
b3515	3664618	3663890	<i>gadW</i>	transcriptional activator of gadA and gadBC; repressor of gadX	0	0
b3516	3665810	3664986	<i>gadX</i>	acid resistance regulon transcriptional activator; autoactivator	0	1
b3517	3667580	3666180	<i>gadA</i>	glutamate decarboxylase A, PLP-dependent	0	2
b3518	3669188	3667791	<i>yhjA</i>	putative cytochrome C peroxidase	264	525
b3519	3669592	3671241	<i>treF</i>	cytoplasmic trehalase	687	1524
b3520	3671894	3671292	<i>yhjB</i>	putative DNA-binding transcriptional response regulator	61	337
b3521	3672414	3673313	<i>yhjC</i>	LysR family putative transcriptional regulator	162	249
b3522	3673362	3674375	<i>yhjD</i>	inner membrane putative BrbK family alternate lipid exporter	1242	2436
b3523	3674786	3676108	<i>yhjE</i>	putative MFS transporter; membrane protein	47	530
b3524	3678350	3676290	<i>yhjG</i>	putative inner membrane-anchored periplasmic AsmA family protein	1296	1920
b3525	3679187	3678420	<i>yhjH</i>	cyclic-di-GMP phosphodiesterase, FlhDC-regulated	1066	925
b3526	3679419	3680348	<i>kdgK</i>	2-dehydro-3-deoxygluconokinase	889	303
b3527	3681940	3680444	<i>yhjJ</i>	putative periplasmic M16 family chaperone	802	2800
b3528	3683447	3682161	<i>dctA</i>	C4-dicarboxylic acid, orotate and citrate transporter	37469	3986
b3529	3685618	3683630	<i>yhjK</i>	cyclic-di-GMP phosphodiesterase	891	898
b3530	3689173	3685700	<i>bcsC</i>	cellulose synthase subunit	645	806
b3531	3690261	3689155	<i>bcsZ</i>	endo-1,4-D-glucanase	96	106
b3532	3692607	3690268	<i>bcsB</i>	regulator of cellulose synthase, cyclic di-GMP binding	253	197
b3533	3695236	3692618	<i>bcsA</i>	cellulose synthase, catalytic subunit	109	271
b3535	3696185	3695997	<i>yhjR</i>	DUF2629 family protein	127	74
b3536	3696458	3698029	<i>bcsE</i>	cellulose production protein	5598	4879
b3537	3698026	3698217	<i>bcsF</i>	DUF2636 family cellulose production small membrane protein	271	162
b3538	3698214	3699893	<i>bcsG</i>	DUF3260 family cellulose production inner membrane protein	1637	879
b3539	3700563	3701834	<i>yhjV</i>	putative transporter	259	1403
b3540	3702868	3701864	<i>dppF</i>	dipeptide/heme ABC transporter ATPas	470	679
b3541	3703848	3702865	<i>dppD</i>	dipeptide/heme ABC transporter ATPas	324	354

b3542	3704761	3703859	<i>dppC</i>	dipeptide/heme ABC transporter permease	136	190
b3543	3705790	3704771	<i>dppB</i>	dipeptide/heme ABC transporter permease	151	202
b3544	3707705	3706098	<i>dppA</i>	dipeptide/heme ABC transporter periplasmic binding protein; dipeptide chemotaxis receptor	10166	15019
b3546	3710475	3708784	<i>eptB</i>	KDO phosphoethanolamine transferase, Ca(2+)-inducible	1042	4249
b3547	3712007	3710799	<i>yhjX</i>	pyruvate-inducible inner membrane protein, putative transporter	59	460
b3548	3712934	3712236	<i>yhjY</i>	autotransporter beta-domain protein	1175	1323
b3549	3713092	3713655	<i>tag</i>	3-methyl-adenine DNA glycosylase I, constitutive	410	453
b3550	3713652	3714092	<i>yiaC</i>	GNAT family putative N-acetyltransferase	197	204
b3551	3716394	3714061	<i>bisC</i>	biotin sulfoxide reductase	765	1106
b3552	3716547	3717206	<i>yiaD</i>	multicopy suppressor of bamB; outer membrane lipoprotein	1539	284
b3553	3717310	3718284	<i>ghrB</i>	glyoxylate/hydroxypyruvate reductase B	1450	1808
b3554	3719044	3718334	<i>yiaF</i>	barrier effect co-colonization resistance factor; DUF3053 family lipoprotein	4403	2561
b3555	3719478	3719768	<i>yiaG</i>	HTH_CROC1 family putative transcriptional regulator	1327	3210
b3556	3720049	3720261	<i>cspA</i>	RNA chaperone and antiterminator, cold-inducible	7624	2959
b3557	3720680	3721201	<i>insJ</i>	IS150 transposase A	36	207
b3558	3721198	3722049	<i>insK</i>	IS150 transposase B	71	1687
b3559	3724397	3722328	<i>glyS</i>	glycine tRNA synthetase, beta subunit	8442	3197
b3560	3725318	3724407	<i>glyQ</i>	glycine tRNA synthetase, alpha subunit	4673	2032
b3561	3725887	3726882	<i>wecH</i>	O-acetyltransferase for enterobacterial common antigen (ECA)	106	481
b3562	3727361	3726924	<i>yiaA</i>	YiaAB family inner membrane protein, tandem domains	19	360
b3563	3727748	3727407	<i>yiaB</i>	YiaAB family inner membrane protein	12	193
b3564	3729371	3727917	<i>xylB</i>	xylulokinase	484	273
b3565	3730765	3729443	<i>xylA</i>	D-xylulose isomerase	416	411
b3566	3731131	3732123	<i>xylF</i>	D-xylulose transporter subunit	469	1004
b3567	3732201	3733742	<i>xylG</i>	D-xylulose ABC transporter dual domain ATPase	196	725
b3568	3733720	3734901	<i>xylH</i>	D-xylulose ABC transporter permease	101	248
b3569	3734979	3736157	<i>xylR</i>	xylose divergent operon transcriptional activator	278	1047
b3570	3737177	3736353	<i>bax</i>	putative glucosaminidase	705	13447
b3571	3737497	3739527	<i>malS</i>	alpha-amylase	1346	1647
b3572	3739705	3740958	<i>avtA</i>	valine-pyruvate aminotransferase; transaminase C; alanine-valine transaminase	836	1509
b3573	3741582	3741109	<i>ysaA</i>	putative hydrogenase, 4Fe-4S ferredoxin-type component	1528	484
b3574	3742532	3741684	<i>yiaJ</i>	transcriptional repressor for the yiaKLMNO-lyxK-sgbHUE operon	346	851
b3575	3742733	3743731	<i>yiaK</i>	2,3-diketo-L-gulonate reductase, NADH-dependent	124	169
b3576	3743743	3744210	<i>yiaL</i>	DUF386 family protein	28	106
b3577	3744328	3744801	<i>yiaM</i>	2,3-diketo-L-gulonate TRAP transporter small permease protein	8	69
b3578	3744804	3746081	<i>yiaN</i>	2,3-diketo-L-gulonate TRAP transporter large permease protein	19	267
b3579	3746094	3747080	<i>yiaO</i>	2,3-diketo-L-gulonate-binding periplasmic protein	41	62
b3580	3747084	3748580	<i>lyxK</i>	L-xylulose kinase	32	63
b3581	3748577	3749239	<i>sgbH</i>	3-keto-L-gulonate 6-phosphate decarboxylase	14	22
b3582	3749232	3750092	<i>sgbU</i>	putative L-xylulose 5-phosphate 3-epimerase	23	81
b3583	3750086	3750781	<i>sgbE</i>	L-ribulose-5-phosphate 4-epimerase	40	104
b3584	3751868	3751128	<i>yiaT</i>	putative outer membrane protein	24	302
b3585	3751992	3752966	<i>yiaU</i>	putative DNA-binding transcriptional regulator	362	1724
b3586	3754099	3752963	<i>yiaV</i>	signal-anchored membrane fusion protein (MFP) component of efflux pump	32	415
b3587	3754428	3754105	<i>yiaW</i>	DUF3302 family inner membrane protein	2	100
b3588	3756511	3754973	<i>aldB</i>	aldehyde dehydrogenase B	1643	1040
b3589	3757827	3756676	<i>yiaY</i>	L-threonine dehydrogenase	10	100

b3590	3759861	3758017	<i>selB</i>	selenocysteinyl-tRNA-specific translation factor	1913	841
b3591	3761249	3759858	<i>selA</i>	selenocysteine synthase	1570	798
b3592	3761955	3761347	<i>yibF</i>	glutathione S-transferase homolog	154	180
b3593	3762183	3766316	<i>rhsA</i>	Rhs protein with putative toxin 55 domain; putative polysaccharide synthesis/export protein; putative neighboring cell growth inhibitor	709	851
b3594	3766337	3767179	<i>yibA</i>	putative immunity protein for polymorphic toxin RhsA; HEAT-domain protein; lethality reduction protein	774	4189
b3596	3768177	3768638	<i>yibG</i>	TPR-like repeat protein	71	379
b3597	3771379	3770243	<i>yibH</i>	putative membrane fusion protein (MFP) component of efflux pump	390	223
b3598	3771744	3771382	<i>yibI</i>	DUF3302 family inner membrane protein	307	281
b3599	3772281	3774194	<i>mtlA</i>	mannitol-specific PTS enzyme: IIA, IIB and IIC components	8245	1419
b3600	3774424	3775572	<i>mtlD</i>	mannitol-1-phosphate dehydrogenase, NAD-dependent	2900	971
b3601	3775572	3776159	<i>mtlR</i>	mannitol operon repressor	1252	1380
b3602	3776665	3777027	<i>yibL</i>	ribosome-associated DUF2810 family protein	708	661
b3603	3777399	3779054	<i>lldP</i>	L-lactate permease	12582	1399
b3604	3779054	3779830	<i>lldR</i>	dual role activator/repressor for lldPRD operon	2940	463
b3605	3779827	3781017	<i>lldD</i>	L-lactate dehydrogenase, FMN-linked	5436	527
b3606	3781215	3781688	<i>trmL</i>	tRNA Leu mC34,mU34 2'-O-methyltransferase, SAM-dependent	177	159
b3607	3782562	3781741	<i>cysE</i>	serine acetyltransferase	1063	713
b3608	3783661	3782642	<i>gpsA</i>	glycerol-3-phosphate dehydrogenase (NAD ⁺)	4368	1552
b3609	3784128	3783661	<i>secB</i>	protein export chaperone	8929	1929
b3610	3784442	3784191	<i>grxC</i>	glutaredoxin 3	1487	573
b3611	3785015	3784584	<i>yibN</i>	putative rhodanese-related sulfurtransferase	2290	719
b3612	3785260	3786804	<i>gpmM</i>	phosphoglycero mutase III, cofactor-independent	23354	1276
b3613	3786838	3788097	<i>envC</i>	activator of AmiB,C murein hydrolases, septal ring factor	710	852
b3614	3788101	3789060	<i>yibQ</i>	putative polysaccharide deacetylase	682	1112
b3615	3790081	3789047	<i>waaH</i>	LPS(HepIII)-glucuronic acid glycosyltransferase	24082	28717
b3616	3791345	3790320	<i>tdh</i>	L-threonine 3-dehydrogenase, NAD(P)-binding	26691	2683
b3617	3792551	3791355	<i>kbl</i>	glycine C-acetyltransferase	24353	1898
b3618	3793683	3792826	<i>yibB</i>	YibB family protein, function unknown	2605	7120
b3619	3793987	3794919	<i>hldD</i>	ADP-L-glycero-D-mannoheptose-6-epimerase, NAD(P)-binding	5559	2155
b3620	3794929	3795975	<i>waaF</i>	ADP-heptose:LPS heptosyltransferase II	1417	653
b3621	3795979	3796938	<i>waaC</i>	ADP-heptose:LPS heptosyl transferase I	774	1978
b3622	3796948	3798207	<i>waaL</i>	O-antigen ligase	3375	21244
b3623	3799312	3798239	<i>waaU</i>	lipopolysaccharide core biosynthesis	2260	25950
b3624	3800196	3799345	<i>waaZ</i>	lipopolysaccharide KdoIII transferase; lipopolysaccharide core biosynthesis protein	780	3714
b3625	3800965	3800267	<i>waaY</i>	lipopolysaccharide core biosynthesis protein	746	3395
b3626	3801999	3800983	<i>waaR</i>	lipopolysaccharide 1,2-glucosyltransferase; UDP-glucose:(glucosyl)LPS alpha-1,2-glucosyltransferase	1742	8914
b3627	3803058	3802039	<i>waaO</i>	UDP-D-galactose:(glucosyl)lipopolysaccharide- alpha-1,3-D-galactosyltransferase	2181	7870
b3628	3804137	3803058	<i>waaB</i>	lipopolysaccharide 1,6-galactosyltransferase; UDP-D-galactose:(glucosyl)lipopolysaccharide-1, 6-D-galactosyltransferase	2242	7503
b3629	3805116	3804181	<i>waaS</i>	lipopolysaccharide rhamnose:KdoIII transferase; lipopolysaccharide core biosynthesis protein	2343	26542
b3630	3805950	3805153	<i>waaP</i>	kinase that phosphorylates core heptose of lipopolysaccharide	848	2722
b3631	3807067	3805943	<i>waaG</i>	UDP-glucose:(heptosyl)lipopolysaccharide alpha-1,3-glucosyltransferase; lipopolysaccharide core biosynthesis protein; lipopolysaccharide glucosyltransferase I	1386	3601
b3632	3808098	3807064	<i>waaQ</i>	lipopolysaccharide core biosynthesis protein	934	2610
b3633	3808540	3809817	<i>waaA</i>	3-deoxy-D-manno-octulosonic-acid transferase (KDO transferase)	1024	1032

b3634	3809825	3810304	<i>coaD</i>	pantetheine-phosphate adenylyltransferase	706	242
b3635	3811152	3810343	<i>mutM</i>	formamidopyrimidine/5-formyluracil/ 5-hydroxymethyluracil DNA glycosylase	840	424
b3636	3811417	3811250	<i>rpmG</i>	50S ribosomal subunit protein L33	9441	4542
b3637	3811674	3811438	<i>rpmB</i>	50S ribosomal subunit protein L28	6079	1831
b3638	3812559	3811891	<i>yicR</i>	UPF0758 family protein	833	539
b3639	3812731	3813951	<i>dfp</i>	fused 4'-phosphopantothenoylcysteine decarboxylase/phosphopantothenoylcysteine synthetase, FMN-binding	2320	1180
b3640	3813932	3814387	<i>dut</i>	deoxyuridinetriphosphatase	1114	584
b3641	3814494	3815090	<i>slmA</i>	nucleoid occlusion factor, anti-FtsZ division inhibitor	1695	584
b3642	3815768	3815127	<i>pyrE</i>	orotate phosphoribosyltransferase	1594	221
b3644	3816676	3817539	<i>yicC</i>	UPF0701 family protein	4048	1307
b3645	3817760	3818584	<i>dinD</i>	DNA damage-inducible protein	1192	5482
b3646	3818874	3819491	<i>yicG</i>	UPF0126 family inner membrane protein	472	384
b3647	3821170	3819488	<i>ligB</i>	DNA ligase, NAD(+)-dependent	378	578
b3648	3821428	3822051	<i>gmk</i>	guanylate kinase	2133	13324
b3649	3822106	3822381	<i>rpoZ</i>	RNA polymerase, omega subunit	693	972
b3650	3822400	3824508	<i>spoT</i>	bifunctional (p)ppGpp synthetase II/ guanosine-3',5'-bis pyrophosphate 3'-pyrophosphohydrolase	2886	2490
b3651	3824515	3825204	<i>trmH</i>	tRNA mG18-2'-O-methyltransferase, SAM-dependent	333	322
b3652	3825210	3827291	<i>recG</i>	ATP-dependent DNA helicase	671	490
b3653	3828665	3827460	<i>gltS</i>	glutamate transporter	1986	525
b3654	3828945	3830336	<i>xanP</i>	xanthine permease	213	281
b3655	3830457	3832166	<i>yicH</i>	putative inner membrane-anchored periplasmic AsmA family protein	1302	1526
b3656	3834537	3832219	<i>yicI</i>	putative alpha-glucosidase	354	399
b3657	3835929	3834547	<i>yicJ</i>	putative transporter	71	303
b3659	3836953	3838137	<i>setC</i>	putative arabinose efflux transporter	10	215
b3660	3838248	3839171	<i>yicL</i>	EamA family inner membrane putative transporter	379	743
b3661	3839993	3839175	<i>nlpA</i>	cytoplasmic membrane lipoprotein-28	2542	1774
b3662	3841739	3840549	<i>nepI</i>	putative transporter	44	246
b3663	3842402	3841950	<i>yicN</i>	DUF1198 family protein	98	93
b3664	3843789	3842455	<i>adeQ</i>	adenine permease, high affinity; adenine:H ⁺ symporter	32	260
b3665	3843964	3845730	<i>adeD</i>	cryptic adenine deaminase	1059	349
b3666	3847167	3845776	<i>uhpT</i>	hexose phosphate transporter	419	535
b3667	3848624	3847305	<i>uhpC</i>	membrane protein regulates uhpT expression	106	293
b3668	3850136	3848634	<i>uhpB</i>	sensory histidine kinase in two-component regulatory system with UhpA	73	157
b3669	3850726	3850136	<i>uhpA</i>	response regulator in two-component regulatory system with UhpB	55	151
b3670	3851092	3850802	<i>ilvN</i>	acetolactate synthase 1 small subunit	172	378
b3671	3852784	3851096	<i>ilvB</i>	acetolactate synthase 2 large subunit	779	1994
b3672	3852988	3852890	<i>ivbL</i>	ilvB operon leader peptide	1	12
b3673	3853922	3855106	<i>emrD</i>	multidrug efflux system protein	390	222
b3674	3855611	3855114	<i>yidF</i>	putative Cys-type oxidative YidJ-maturing enzyme	960	1065
b3675	3855970	3855608	<i>yidG</i>	inner membrane protein	50	80
b3676	3856307	3855960	<i>yidH</i>	DUF202 family inner membrane protein	64	63
b3677	3856415	3856864	<i>yidI</i>	inner membrane protein	146	158
b3678	3858404	3856911	<i>yidJ</i>	sulfatase/phosphatase superfamily protein	79	159
b3679	3860116	3858401	<i>yidK</i>	putative transporter	73	132
b3680	3860283	3861176	<i>yidL</i>	AraC family putative transcriptional regulator	236	330
b3684	3863899	3864615	<i>yidP</i>	UTRA domain-containing GntR family putative transcriptional regulator	57	229
b3685	3866273	3864612	<i>yidE</i>	putative transporter	7244	669
b3686	3866897	3866469	<i>ibpB</i>	heat shock chaperone	8172	4171

b3687	3867422	3867009	<i>ibpA</i>	heat shock chaperone	5535	3735
b3688	3867728	3868060	<i>vidQ</i>	DUF1375 family outer membrane protein	1978	2908
b3689	3869309	3868062	<i>vidR</i>	DUF3748 family protein	578	527
b3690	3869377	3870441	<i>cbrA</i>	colicin M resistance protein; FAD-binding protein, putative oxidoreductase	136	182
b3691	3871730	3870438	<i>dgoT</i>	D-galactonate transporter	38	237
b3693	3874474	3873596	<i>dgoK</i>	2-oxo-3-deoxygalactonate kinase	221	163
b3696	3875438	3876094	<i>yidX</i>	putative lipoprotein	138	929
b3697	3876952	3876140	<i>yidA</i>	sugar phosphate phosphatase	2671	777
b3698	3877465	3877067	<i>yidB</i>	DUF937 family protein	304	623
b3699	3880119	3877705	<i>gyrB</i>	DNA gyrase, subunit B	11523	7530
b3700	3881221	3880148	<i>recF</i>	gap repair protein	333	428
b3701	3882321	3881221	<i>dnaN</i>	DNA polymerase III, beta subunit	1948	1466
b3702	3883729	3882326	<i>dnaA</i>	chromosomal replication initiator protein DnaA, DNA-binding transcriptional dual regulator	2119	1393
b3703	3884336	3884476	<i>rpmH</i>	50S ribosomal subunit protein L34	538	272
b3704	3884493	3884852	<i>rnpA</i>	protein C5 component of RNase P	804	301
b3705	3885076	3886722	<i>yidC</i>	membrane protein insertase	9891	2709
b3706	3886828	3888192	<i>nmnE</i>	tRNA U34 5-methylaminomethyl-2-thiouridine modification GTPase	1333	720
b3707	3888435	3888509	<i>tnaC</i>	tryptophanase leader peptide	31	43
b3708	3888730	3890145	<i>tnaA</i>	tryptophanase/L-cysteine desulfhydrase, PLP-dependent	61957	13336
b3709	3890236	3891483	<i>tnaB</i>	tryptophan transporter of low affinity	4712	3344
b3710	3891615	3892790	<i>mdtL</i>	multidrug efflux system protein	105	233
b3711	3892765	3893724	<i>yidZ</i>	putative DNA-binding transcriptional regulator	622	808
b3712	3893881	3894630	<i>yieE</i>	phosphopantetheinyl transferase superfamily protein	1498	535
b3713	3894652	3895218	<i>chrR</i>	chromate reductase, Class I, flavoprotein	2490	340
b3714	3896609	3895272	<i>adeP</i>	adenine permease, high affinity; adenine:H ⁺ symporter	1225	810
b3715	3896774	3897439	<i>yieH</i>	phosphoenolpyruvate and 6-phosphogluconate phosphatase	175	496
b3716	3897506	3897973	<i>cbrB</i>	PRK09823 family inner membrane protein, creBC regulon	417	1563
b3717	3898022	3898609	<i>cbrC</i>	UPF0167 family protein	660	1289
b3718	3899393	3898671	<i>yieK</i>	putative 6-phosphogluconolactonase	136	263
b3719	3900577	3899408	<i>yieL</i>	putative xylanase	121	177
b3720	3902220	3900604	<i>bglH</i>	carbohydrate-specific outer membrane porin, cryptic	34	283
b3721	3903701	3902289	<i>bglB</i>	cryptic phospho-beta-glucosidase B	55	241
b3722	3905597	3903720	<i>bglF</i>	fused beta-glucoside-specific PTS enzymes: IIA component/IIB component/IIC component	361	969
b3723	3906567	3905731	<i>bglG</i>	transcriptional antiterminator of the bgl operon	70	485
b3724	3907578	3906853	<i>phoU</i>	negative regulator of PhoR/PhoB two-component regulator	3060	1085
b3725	3908366	3907593	<i>pstB</i>	phosphate ABC transporter ATPase	2226	1993
b3726	3909439	3908549	<i>pstA</i>	phosphate ABC transporter permease	488	639
b3727	3910398	3909439	<i>pstC</i>	phosphate ABC transporter permease	976	1978
b3728	3911525	3910485	<i>pstS</i>	phosphate ABC transporter periplasmic binding protein	11981	11708
b3729	3913668	3911839	<i>glmS</i>	L-glutamine:D-fructose-6-phosphate aminotransferase	16222	3175
b3730	3915200	3913830	<i>glmU</i>	fused N-acetyl glucosamine-1-phosphate uridylyltransferase/glucosamine-1-phosphate acetyl transferase	5494	1891
b3731	3915972	3915553	<i>atpC</i>	F1 sector of membrane-bound ATP synthase, epsilon subunit	22241	3537
b3732	3917375	3915993	<i>atpD</i>	F1 sector of membrane-bound ATP synthase, beta subunit	65687	5273
b3733	3918265	3917402	<i>atpG</i>	F1 sector of membrane-bound ATP synthase, gamma subunit	40329	6138
b3734	3919857	3918316	<i>atpA</i>	F1 sector of membrane-bound ATP synthase, alpha subunit	101534	12132

b3735	3920403	3919870	<i>atpH</i>	F1 sector of membrane-bound ATP synthase, delta subunit	10207	1817
b3736	3920888	3920418	<i>atpF</i>	F0 sector of membrane-bound ATP synthase, subunit b	15913	6247
b3737	3921189	3920950	<i>atpE</i>	F0 sector of membrane-bound ATP synthase, subunit c	3928	1506
b3738	3922051	3921236	<i>atpB</i>	F0 sector of membrane-bound ATP synthase, subunit a	9029	2542
b3739	3922440	3922060	<i>atpI</i>	ATP synthase, membrane-bound accessory factor	3360	2187
b3740	3923680	3923057	<i>rsmG</i>	16S rRNA m(7)G527 methyltransferase, SAM-dependent; glucose-inhibited cell-division protein	791	743
b3741	3925633	3923744	<i>mnmG</i>	5-methylaminomethyl-2-thiouridine modification at tRNA U34	2738	2334
b3742	3926455	3926012	<i>mioC</i>	FMN-binding protein MioC	2150	3873
b3743	3927003	3926545	<i>asnC</i>	transcriptional activator of <i>asnA</i> ; autorepressor	256	842
b3744	3927155	3928147	<i>asnA</i>	asparagine synthetase A	4548	2598
b3745	3929603	3928152	<i>viaA</i>	stimulator of RavA ATPase activity; von Willebrand factor domain protein	1147	789
b3746	3931093	3929597	<i>ravA</i>	hexameric AAA+ MoxR family ATPase, putative molecular chaperone	3033	1161
b3747	3931316	3933184	<i>kup</i>	potassium transporter	921	932
b3748	3933351	3933770	<i>rbsD</i>	D-ribose pyranase	12321	130465
b3749	3933778	3935283	<i>rbsA</i>	D-ribose ABC transporter ATPase	4538	11501
b3750	3935288	3936253	<i>rbsC</i>	D-ribose ABC transporter permease	2697	6050
b3751	3936278	3937168	<i>rbsB</i>	D-ribose ABC transporter periplasmic binding protein; ribose chemotaxis receptor	12007	13035
b3752	3937294	3938223	<i>rbsK</i>	ribokinase	2986	1669
b3753	3938227	3939219	<i>rbsR</i>	transcriptional repressor of ribose metabolism	1032	1361
b3754	3940612	3939185	<i>hsrA</i>	putative multidrug or homocysteine efflux system	2128	1411
b3755	3941327	3940635	<i>yieP</i>	putative transcriptional regulator	5960	3483
b3764	3948086	3948424	<i>yifE</i>	UPF0438 family protein	8004	6413
b3765	3949969	3948449	<i>yifB</i>	magnesium chelatase family protein and putative transcriptional regulator	328	812
b3766	3950322	3950420	<i>ilvL</i>	ilvG operon leader peptide	12	94
b3769	3952201	3952464	<i>ilvM</i>	acetolactate synthase 2 small subunit	12	33
b3770	3952484	3953413	<i>ilvE</i>	branched-chain amino acid aminotransferase	731	354
b3771	3953478	3955328	<i>ilvD</i>	dihydroxyacid dehydratase	545	340
b3772	3955331	3956875	<i>ilvA</i>	l-threonine dehydratase, biosynthetic; also known as threonine deaminase	255	138
b3773	3957820	3956927	<i>ilvY</i>	transcriptional activator of <i>ilvC</i> ; autorepressor	174	109
b3774	3957970	3959445	<i>ilvC</i>	ketol-acid reductoisomerase, NAD(P)-binding	1296	6138
b3775	3959813	3959532	<i>ppiC</i>	peptidyl-prolyl cis-trans isomerase C (rotamase C)	1009	379
b3778	3960677	3962698	<i>rep</i>	DNA helicase and single-stranded DNA-dependent ATPase	1032	733
b3779	3964229	3962745	<i>gpp</i>	guanosine pentaphosphatase/exopolyphosphatase	1134	861
b3780	3965630	3964365	<i>rhlB</i>	ATP-dependent RNA helicase	4617	3250
b3781	3965761	3966090	<i>trxA</i>	thioredoxin 1	9579	3663
b3783	3966417	3967676	<i>rho</i>	transcription termination factor	14668	13582
b3784	3967916	3969019	<i>wecA</i>	UDP-GlcNAc:undecaprenylphosphate GlcNAc-1-phosphate transferase	2294	1496
b3785	3969031	3970077	<i>wzzE</i>	Entobacterial Common Antigen (ECA) polysaccharide chain length modulation protein	1942	928
b3786	3970133	3971263	<i>wecB</i>	UDP-N-acetyl glucosamine-2-epimerase	1956	843
b3787	3971260	3972522	<i>wecC</i>	UDP-N-acetyl-D-mannosaminuronic acid dehydrogenase	1597	381
b3788	3972522	3973589	<i>rffG</i>	dTDP-glucose 4,6-dehydratase	1524	433
b3789	3973608	3974489	<i>rffH</i>	glucose-1-phosphate thymidyltransferase	989	238
b3790	3974467	3975141	<i>wecD</i>	TDP-fucosamine acetyltransferase	456	146
b3791	3975146	3976276	<i>wecE</i>	TDP-4-oxo-6-deoxy-D-glucose transaminase	2010	344
b3792	3976278	3977528	<i>wzxE</i>	O-antigen translocase	647	416
b3793	3978601	3979953	<i>wzyE</i>	putative ECA polysaccharide chain elongation protein	246	422
b3794	3979956	3980696	<i>wecG</i>	UDP-N-acetyl-D-mannosaminuronic acid transferase	520	413

b3795	3980887	3982272	<i>yifK</i>	putative APC family amino acid transporter	701	280
b3800	3982958	3984193	<i>aslB</i>	putative AslA-specific sulfatase-maturating enzyme	149	112
b3801	3986007	3984352	<i>aslA</i>	putative Ser-type periplasmic non-aryl sulfatase	285	685
b3802	3987882	3986686	<i>hemY</i>	putative protoheme IX synthesis protein	2500	1403
b3803	3989066	3987885	<i>hemX</i>	putative uroporphyrinogen III methyltransferase	2903	1291
b3804	3989828	3989088	<i>hemD</i>	uroporphyrinogen III synthase	680	706
b3805	3990766	3989825	<i>hemC</i>	hydroxymethylbilane synthase	1377	609
b3806	3991153	3993699	<i>cyaA</i>	adenylate cyclase	3503	6993
b3807	3994059	3993739	<i>cyaY</i>	iron-dependent inhibitor of iron-sulfur cluster formation; frataxin; iron-binding and oxidizing protein	325	575
b3809	3994762	3995586	<i>dapF</i>	diaminopimelate epimerase	1487	492
b3810	3995583	3996290	<i>yigA</i>	DUF484 family protein	898	398
b3811	3996287	3997183	<i>xerC</i>	site-specific tyrosine recombinase	1233	385
b3812	3997183	3997899	<i>yigB</i>	5-amino-6-(5-phospho-D-ribitylamino)uracil phosphatase; pyrimidine phosphatase; riboflavin synthesis	867	292
b3813	3997983	4000145	<i>uvrD</i>	DNA-dependent ATPase I and helicase II	1198	1492
b3816	4001426	4002376	<i>corA</i>	magnesium/nickel/cobalt transporter	3486	2850
b3817	4002799	4002419	<i>yigF</i>	DUF2628 family putative inner membrane protein	106	370
b3818	4003193	4002813	<i>yigG</i>	PRK11371 family inner membrane protein	13	279
b3819	4004178	4003288	<i>rarD</i>	putative chloramphenicol resistance permease	411	306
b3820	4004697	4004230	<i>yigI</i>	4HBT thioesterase family protein	425	300
b3821	4004862	4005731	<i>pldA</i>	outer membrane phospholipase A	1487	903
b3822	4005864	4007693	<i>recQ</i>	ATP-dependent DNA helicase	698	792
b3823	4007757	4008377	<i>rhtC</i>	threonine efflux pump	260	282
b3824	4009059	4008439	<i>rhtB</i>	homoserine, homoserine lactone and S-methyl-methionine efflux pump	195	333
b3825	4009170	4010192	<i>pldB</i>	lysophospholipase L2	1211	895
b3826	4010200	4011000	<i>yigL</i>	pyridoxal phosphate phosphatase	1228	797
b3827	4011076	4011975	<i>yigM</i>	putative inner membrane EamA-like transporter	484	729
b3828	4012816	4011863	<i>metR</i>	methionine biosynthesis regulon transcriptional regulator	1123	2576
b3829	4013053	4015314	<i>metE</i>	5-methyltetrahydropteroyltrimethylglutamate- homocysteine S-methyltransferase	5294	6466
b3830	4016169	4015354	<i>ysgA</i>	putative carboxymethylenebutenolidase	983	973
b3831	4016431	4017192	<i>udp</i>	uridine phosphorylase	8783	785
b3832	4017333	4018760	<i>rmuC</i>	DNA recombination protein	1493	1521
b3833	4018855	4019610	<i>ubiE</i>	bifunctional 2-octaprenyl-6-methoxy-1,4-benzoquinone methylase/ S-adenosylmethionine:2-DMK methyltransferase	2383	862
b3834	4019624	4020229	<i>ubiJ</i>	aerobic ubiquinone synthesis protein, SCP2 family protein	676	275
b3835	4020226	4021866	<i>ubiB</i>	regulator of octaprenylphenol hydroxylation, ubiquinone synthesis; regulator of 2'-N-acetyltransferase; putative ABC1 family protein kinase	2005	1806
b3836	4021945	4022214	<i>tatA</i>	TatABCE protein translocation system subunit	5728	11072
b3838	4022218	4022733	<i>tatB</i>	TatABCE protein translocation system subunit	2801	1524
b3839	4022736	4023512	<i>tatC</i>	TatABCE protein translocation system subunit	797	479
b3842	4024821	4024333	<i>rfaH</i>	transcription antitermination protein	530	462
b3843	4024988	4026481	<i>ubiD</i>	3-octaprenyl-4-hydroxybenzoate decarboxylase	11251	2953
b3844	4026527	4027228	<i>fre</i>	NAD(P)H-flavin reductase	4167	885
b3845	4028772	4027609	<i>fadA</i>	3-ketoacyl-CoA thiolase (thiolase I)	5183	2678
b3846	4030971	4028782	<i>fadB</i>	fused 3-hydroxybutyryl-CoA epimerase/delta(3)-cis-delta(2)-trans-enoyl-CoA isomerase/enoyl-CoA hydratase/3-hydroxyacyl-CoA dehydrogenase	38777	15915
b3847	4031161	4032492	<i>pepQ</i>	proline dipeptidase	5732	2076
b3848	4032492	4033106	<i>yigZ</i>	UPF0029 family protein	452	186
b3849	4033145	4034596	<i>trkH</i>	potassium transporter	904	839

b3850	4034608	4035153	<i>hemG</i>	protoporphyrin oxidase, flavoprotein	620	418
b3856	4041433	4040906	<i>mobB</i>	molybdopterin-guanine dinucleotide biosynthesis protein B	175	256
b3857	4041999	4041415	<i>mobA</i>	molybdopterin-guanine dinucleotide synthase	187	279
b3858	4042069	4042338	<i>yihD</i>	DUF1040 protein YihD	461	355
b3859	4042415	4043401	<i>srkA</i>	Cpx stress response Thr/Ser protein kinase; MazF antagonist protein	572	1611
b3860	4043418	4044044	<i>dsbA</i>	periplasmic protein disulfide isomerase I	6420	5276
b3861	4044199	4045629	<i>yihF</i>	DUF945 family protein	132	1541
b3862	4046602	4045670	<i>yihG</i>	inner membrane protein, inner membrane acyltransferase	154	642
b3863	4046966	4049752	<i>polA</i>	5' to 3' DNA polymerase and 3' to 5'/5' to 3' exonuclease	8990	4559
b3865	4050765	4050133	<i>yihA</i>	cell division GTP-binding protein	2799	1434
b3866	4051347	4051856	<i>yihI</i>	activator of Der GTPase	2255	1760
b3867	4052045	4053418	<i>hemN</i>	coproporphyrinogen III oxidase, SAM and NAD(P)H dependent, oxygen-independent	2131	1781
b3868	4055278	4053869	<i>glnG</i>	fused DNA-binding response regulator in two-component regulatory system with GlnL: response regulator/sigma54 interaction protein	739	442
b3869	4056339	4055290	<i>glnL</i>	sensory histidine kinase in two-component regulatory system with GlnG	405	569
b3870	4058034	4056625	<i>glnA</i>	glutamine synthetase	10556	7015
b3871	4058407	4060230	<i>typA</i>	GTP-binding protein	31587	4891
b3872	4060447	4061157	<i>yihL</i>	putative DNA-binding transcriptional regulator	497	151
b3873	4061165	4062145	<i>yihM</i>	putative sugar phosphate isomerase	966	404
b3874	4062247	4063512	<i>yihN</i>	MFS transporter family protein	411	262
b3875	4064295	4063603	<i>ompL</i>	outer membrane porin L; putative sulpholipid porin	18	369
b3876	4065766	4064363	<i>yihO</i>	putative sulphoquinovose importer	58	407
b3877	4067194	4065809	<i>yihP</i>	putative 2,3-dihydroxypropane-1-sulphonate exporter, membrane protein	41	245
b3878	4069276	4067240	<i>yihQ</i>	putative sulpholipid alpha-glucosidase; alpha-glucosyl fluoride glucosidase	45	132
b3879	4070401	4069475	<i>yihR</i>	putative sulphoquinovose mutarotase	25	69
b3880	4071756	4070515	<i>yihS</i>	sulphoquinovose isomerase	73	190
b3881	4072651	4071773	<i>yihT</i>	6-deoxy-6-sulphofructose-1-phosphate aldolase	31	88
b3882	4073571	4072675	<i>yihU</i>	3-sulpholactaldehyde (SLA) reductase, NADH-dependent; gamma-hydroxybutyrate dehydrogenase, NADH-dependent	18	26
b3883	4073739	4074635	<i>yihV</i>	6-deoxy-6-sulphofructose kinase	155	87
b3884	4074669	4075454	<i>yihW</i>	putative transcriptional regulator for sulphoquinovose utilization	2961	1105
b3885	4075553	4076152	<i>yihX</i>	alpha-D-glucose-1-phosphate phosphatase, anomer-specific	3220	1508
b3886	4076146	4077018	<i>yihY</i>	BrkB family putative transporter, inner membrane protein	1530	1083
b3887	4077015	4077452	<i>dtd</i>	D-tyr-tRNA(Tyr) deacylase	684	1317
b3888	4077449	4078438	<i>yiiD</i>	GNAT family putative N-acetyltransferase	1317	1589
b3889	4079297	4079509	<i>yiiE</i>	CopG family putative transcriptional regulator	15	108
b3890	4079751	4079969	<i>yiiF</i>	putative thymol sensitivity protein, CopG family putative transcriptional regulator	125	86
b3891	4081228	4080299	<i>fdhE</i>	formate dehydrogenase formation protein	2172	915
b3892	4081860	4081225	<i>fdoI</i>	formate dehydrogenase-O, cytochrome b556 subunit	2757	1937
b3893	4082759	4081857	<i>fdoH</i>	formate dehydrogenase-O, Fe-S subunit	3985	2470
b3894	4085822	4082772	<i>fdoG</i>	formate dehydrogenase-O, large subunit	30288	11049
b3895	4086016	4086849	<i>fdhD</i>	formate dehydrogenase formation protein	662	414
b3896	4087002	4088057	<i>yiiG</i>	DUF3829 family lipoprotein	100	161
b3897	4089855	4088107	<i>frvR</i>	putative frv operon regulator; contains a PTS EIIA domain	169	162
b3898	4090925	4089855	<i>frvX</i>	putative peptidase	101	191
b3899	4092366	4090915	<i>frvB</i>	putative PTS enzyme, IIB component/IIC component	56	94
b3900	4092823	4092377	<i>frvA</i>	putative enzyme IIA component of PTS	55	26

b3901	4093438	4093124	<i>rhaM</i>	L-rhamnose mutarotase	12	27
b3902	4094272	4093448	<i>rhaD</i>	rhamnulose-1-phosphate aldolase	32	97
b3903	4095982	4094723	<i>rhaA</i>	L-rhamnose isomerase	26	43
b3904	4097448	4095979	<i>rhaB</i>	rhamnulokinase	33	83
b3905	4097736	4098572	<i>rhaS</i>	transcriptional activator of rhaBAD and rhaT	168	118
b3906	4098646	4099494	<i>rhaR</i>	transcriptional activator of rhaSR	428	247
b3907	4100525	4099491	<i>rhaT</i>	L-rhamnose:proton symporter	98	246
b3908	4100810	4101430	<i>sodA</i>	superoxide dismutase, Mn	40077	5638
b3909	4101690	4102673	<i>kdgT</i>	2-keto-3-deoxy-D-gluconate transporter	330	344
b3910	4102822	4103496	<i>yiiM</i>	6-N-hydroxylaminopurine resistance protein	665	536
b3911	4104975	4103602	<i>cpxA</i>	sensory histidine kinase in two-component regulatory system with CpxR	1398	1533
b3912	4105670	4104972	<i>cpxR</i>	response regulator in two-component regulatory system with CpxA	2929	3335
b3915	4106469	4107371	<i>fieF</i>	ferrous iron and zinc transporter	1954	1811
b3916	4107552	4108514	<i>pfkA</i>	6-phosphofructokinase I	17172	2656
b3917	4108834	4109823	<i>sbp</i>	sulfate transporter subunit	5673	2204
b3918	4109930	4110685	<i>cdh</i>	CDP-diacylglycerol phosphatidylhydrolase	252	218
b3919	4111507	4110740	<i>tpiA</i>	triosephosphate isomerase	28154	4726
b3920	4112214	4111615	<i>yiiQ</i>	DUF1454 family putative periplasmic protein	359	531
b3921	4112315	4112755	<i>yiiR</i>	DUF805 family putative inner membrane protein	203	376
b3922	4112967	4113266	<i>yiiS</i>	UPF0381 family protein	827	313
b3923	4113293	4113721	<i>uspD</i>	stress-induced protein	2126	1541
b3924	4114472	4113726	<i>fpr</i>	ferredoxin-NADP reductase; flavodoxin reductase	2267	1015
b3925	4115579	4114569	<i>glpX</i>	fructose 1,6-bisphosphatase II	1507	793
b3926	4117222	4115714	<i>glpK</i>	glycerol kinase	13781	8439
b3927	4118090	4117245	<i>glpF</i>	glycerol facilitator	2840	4711
b3928	4118515	4118760	<i>zapB</i>	FtsZ stabilizer, septal ring assembly factor, cell division stimulator	6493	11226
b3929	4119330	4118845	<i>rraA</i>	ribonuclease E (RNase E) inhibitor protein	13403	7386
b3930	4120349	4119423	<i>menA</i>	1,4-dihydroxy-2-naphthoate octaprenyltransferase	453	264
b3931	4121747	4120416	<i>hslU</i>	molecular chaperone and ATPase component of HslUV protease	18753	4117
b3932	4122287	4121757	<i>hslV</i>	peptidase component of the HslUV protease	3823	1387
b3933	4123339	4122380	<i>ftsN</i>	essential cell division protein	1264	879
b3934	4124456	4123431	<i>cytR</i>	Anti-activator for CytR-CRP nucleoside utilization regulon	2666	687
b3935	4126810	4124612	<i>priA</i>	Primosome factor n' (replication factor Y)	367	358
b3936	4127013	4127225	<i>rpmE</i>	50S ribosomal subunit protein L31	10451	2990
b3937	4127894	4127286	<i>yiiX</i>	putative lipid binding hydrolase, DUF830 family protein	166	778
b3938	4128395	4128078	<i>metJ</i>	transcriptional repressor, S-adenosylmethionine-binding	1778	2957
b3939	4128672	4129832	<i>metB</i>	cystathionine gamma-synthase, PLP-dependent	1609	3991
b3940	4129835	4132267	<i>metL</i>	Bifunctional aspartokinase/homoserine dehydrogenase 2	2081	1766
b3941	4132616	4133506	<i>metF</i>	5,10-methylenetetrahydrofolate reductase	1715	5068
b3942	4133835	4136015	<i>katG</i>	catalase-peroxidase HPI, heme b-containing	12352	2492
b3943	4136108	4137013	<i>yijE</i>	EamA-like transporter family protein	141	275
b3944	4137657	4137040	<i>yijF</i>	DUF1287 family protein	19	164
b3945	4139035	4137932	<i>gldA</i>	glycerol dehydrogenase, NAD+ dependent; 1,2-propanediol:NAD+ oxidoreductase	4489	575
b3946	4139708	4139046	<i>fsaB</i>	fructose-6-phosphate aldolase 2	237	53
b3947	4142221	4139720	<i>frwA</i>	putative PTS enzyme: Hpr, enzyme I and II components	496	114
b3949	4142530	4143609	<i>frwC</i>	putative enzyme IIC component of PTS	82	735
b3950	4143624	4143944	<i>frwB</i>	putative enzyme IIB component of PTS	42	424
b3951	4143995	4146292	<i>pflD</i>	putative glycine radical domain-containing pyruvate formate-lyase	267	188
b3952	4146258	4147136	<i>pflC</i>	putative [formate-C-acetyltransferase 2]-activating	36	137

				enzyme; pyruvate formate-lyase 1-activating enzyme		
b3953	4147138	4147479	<i>frwD</i>	putative enzyme IIB component of PTS	26	112
b3954	4148317	4147466	<i>yijO</i>	AraC family putative transcriptional activator	277	279
b3955	4150265	4148532	<i>eptC</i>	LPS heptose I phosphoethanolamine transferase	11134	6524
b3956	4153098	4150447	<i>ppc</i>	phosphoenolpyruvate carboxylase	6693	3325
b3957	4154847	4153696	<i>argE</i>	acetylornithine deacetylase	821	2149
b3958	4155001	4156005	<i>argC</i>	N-acetyl-gamma-glutamylphosphate reductase, NAD(P)-binding	63	3455
b3959	4156013	4156789	<i>argB</i>	acetylglutamate kinase	131	2679
b3960	4156850	4158223	<i>argH</i>	argininosuccinate lyase	309	2060
b3961	4158490	4159407	<i>oxyR</i>	oxidative and nitrosative stress transcriptional regulator	3143	1292
b3962	4160790	4159390	<i>sthA</i>	pyridine nucleotide transhydrogenase, soluble	18943	5366
b3963	4161124	4161771	<i>fabR</i>	transcriptional repressor of <i>fabA</i> and <i>fabB</i>	8121	9360
b3964	4161771	4162130	<i>yijD</i>	DUF1422 family inner membrane protein	3623	1361
b3965	4163270	4162170	<i>trmA</i>	tRNA m(5)U54 methyltransferase, SAM-dependent; tmRNA m(5)U341 methyltransferase	1888	1777
b3966	4163639	4165483	<i>btuB</i>	vitamin B12/cobalamin outer membrane transporter	14823	2553
b3967	4165428	4166285	<i>murI</i>	glutamate racemase	1857	741
b3972	4172057	4173085	<i>murB</i>	UDP-N-acetylenolpyruvoylglucosamine reductase, FAD-binding	1603	3051
b3973	4173082	4174047	<i>birA</i>	bifunctional biotin-[acetylCoA carboxylase] holoenzyme synthetase/ DNA-binding transcriptional repressor, bio-5'-AMP-binding	1275	1217
b3974	4175026	4174076	<i>coaA</i>	pantothenate kinase	2382	2365
b3980	4175944	4177128	<i>tufB</i>	translation elongation factor EF-Tu 2	96365	17633
b3981	4177358	4177741	<i>secE</i>	preprotein translocase membrane subunit	901	512
b3982	4177743	4178288	<i>nusG</i>	transcription termination factor	3167	1025
b3983	4178447	4178875	<i>rplK</i>	50S ribosomal subunit protein L11	22480	3734
b3984	4178879	4179583	<i>rplA</i>	50S ribosomal subunit protein L1	63113	10154
b3985	4179996	4180493	<i>rplJ</i>	50S ribosomal subunit protein L10	52867	6753
b3986	4180560	4180925	<i>rplL</i>	50S ribosomal subunit protein L7/L12	53176	7148
b3987	4181245	4185273	<i>rpoB</i>	RNA polymerase, beta subunit	81248	15370
b3988	4185350	4189573	<i>rpoC</i>	RNA polymerase, beta prime subunit	88312	13044
b3989	4189786	4190325	<i>yjaZ</i>	stationary phase growth adaptation protein	163	1668
b3990	4191868	4190735	<i>thiH</i>	tyrosine lyase, involved in thiamine-thiazole moiety synthesis	72	217
b3991	4192635	4191865	<i>thiG</i>	thiamine biosynthesis ThiGH complex subunit	30	65
b3992	4193576	4192821	<i>thiF</i>	adenyltransferase, modifies ThiS C-terminus	24	104
b3993	4194204	4193569	<i>thiE</i>	thiamine phosphate synthase (thiamine phosphate pyrophosphorylase)	18	85
b3994	4196099	4194204	<i>thiC</i>	phosphomethylpyrimidine synthase	87	565
b3995	4196808	4196332	<i>rsd</i>	stationary phase protein, binds sigma 70 RNA polymerase subunit	5626	3105
b3996	4196903	4197676	<i>nudC</i>	NADH pyrophosphatase	570	532
b3997	4197716	4198780	<i>hemE</i>	uroporphyrinogen decarboxylase	1755	388
b3998	4198790	4199461	<i>nfi</i>	endonuclease V; deoxyinosine 3' endonuclease	437	239
b3999	4199504	4200094	<i>yjaG</i>	DUF416 domain protein	1015	864
b4000	4200281	4200553	<i>hupA</i>	HU, DNA-binding transcriptional regulator, alpha subunit	38666	7883
b4001	4200566	4201261	<i>yjaH</i>	DUF1481 family putative lipoprotein	611	354
b4002	4201688	4201263	<i>zraP</i>	Zn-dependent periplasmic chaperone	46	79
b4003	4201926	4203323	<i>zraS</i>	sensory histidine kinase in two-component regulatory system with ZraR	1100	334
b4004	4203320	4204645	<i>zraR</i>	fused DNA-binding response regulator in two-component regulatory system with ZraS: response regulator/sigma54 interaction protein	467	161
b4005	4205931	4204642	<i>purD</i>	phosphoribosylglycinamide synthetase phosphoribosylamine-glycine ligase	842	613
b4006	4207532	4205943	<i>purH</i>	IMP cyclohydrolase and	1041	713

				phosphoribosylaminoimidazolecarboxamide formyltransferase		
b4011	4213234	4213617	<i>yjaA</i>	stress-induced protein	55	304
b4012	4214123	4213680	<i>yjaB</i>	GNAT-family putative N-acetyltransferase; acetyl coenzyme A-binding protein	136	448
b4013	4214280	4215209	<i>metA</i>	homoserine O-transsuccinylase	1342	3776
b4014	4215478	4217079	<i>aceB</i>	malate synthase A	2366	2202
b4015	4217109	4218413	<i>aceA</i>	isocitrate lyase	1414	1562
b4016	4218596	4220332	<i>aceK</i>	isocitrate dehydrogenase kinase/phosphatase	213	633
b4017	4222487	4220301	<i>arpA</i>	ankyrin repeat protein	40	855
b4018	4223628	4222804	<i>iclR</i>	transcriptional repressor	1321	883
b4019	4223828	4227511	<i>metH</i>	homocysteine-N5-methyltetrahydrofolate transmethylase, B12-dependent	5164	2873
b4020	4227731	4229362	<i>yjbB</i>	putative Na ⁺ /Pi-cotransporter	641	442
b4021	4230142	4229453	<i>pepE</i>	peptidase E, alpha-aspartyl dipeptidase	2254	190
b4022	4230354	4231226	<i>rluF</i>	23S rRNA pseudouridine(2604) synthase	686	678
b4023	4231631	4231359	<i>yjbD</i>	DUF3811 family protein	736	588
b4024	4233233	4231884	<i>lysC</i>	lysine-sensitive aspartokinase 3	229	1025
b4025	4233758	4235407	<i>pgi</i>	glucosephosphate isomerase	14266	4813
b4026	4235906	4236148	<i>yjbE</i>	extracellular polysaccharide production threonine-rich protein	159	63
b4027	4236262	4236900	<i>yjbF</i>	extracellular polysaccharide production lipoprotein	36	35
b4028	4236897	4237634	<i>yjbG</i>	extracellular polysaccharide export OMA protein	33	23
b4029	4237634	4239730	<i>yjbH</i>	DUF940 family extracellular polysaccharide protein	119	184
b4030	4240325	4240735	<i>psiE</i>	phosphate starvation inducible protein	62	1240
b4031	4242254	4240779	<i>xylE</i>	D-xylose transporter	137	565
b4032	4243516	4242626	<i>malG</i>	maltose transporter subunit	2136	301
b4033	4245075	4243531	<i>malF</i>	maltose transporter subunit	4600	937
b4034	4246419	4245229	<i>malE</i>	maltose transporter subunit	39832	4674
b4035	4246784	4247899	<i>malK</i>	maltose ABC transportor ATPase	6691	877
b4036	4247971	4249311	<i>lamB</i>	maltose outer membrane porin (maltoporin)	40596	4928
b4037	4249554	4250474	<i>malM</i>	maltose regulon periplasmic protein	6247	2167
b4039	4252506	4253003	<i>ubiC</i>	chorismate--pyruvate lyase	2222	2074
b4040	4253016	4253888	<i>ubiA</i>	p-hydroxybenzoate octaprenyltransferase	2199	1222
b4041	4256466	4254043	<i>plsB</i>	glycerol-3-phosphate O-acyltransferase	6245	2327
b4042	4256637	4257005	<i>dgkA</i>	diacylglycerol kinase	2223	945
b4043	4257115	4257723	<i>lexA</i>	transcriptional repressor of SOS regulon	5219	2733
b4044	4257742	4259121	<i>dinF</i>	oxidative stress resistance protein; putative MATE family efflux pump; UV and mitomycin C inducible protein	227	365
b4045	4259237	4259446	<i>yjbJ</i>	stress-induced protein, UPF0337 family	5486	11895
b4046	4260003	4259488	<i>zur</i>	transcriptional repressor, Zn(II)-binding	648	488
b4047	4260321	4260575	<i>yjbL</i>	uncharacterized protein	1	67
b4048	4260599	4261306	<i>yjbM</i>	uncharacterized protein	18	285
b4049	4261669	4262706	<i>dusA</i>	tRNA-dihydrouridine synthase A	608	779
b4050	4262840	4263082	<i>pspG</i>	phage shock protein G	32	1689
b4051	4264231	4263248	<i>qorA</i>	quinone oxidoreductase, NADPH-dependent	2180	2059
b4052	4264314	4265729	<i>dnaB</i>	replicative DNA helicase	1253	889
b4053	4265782	4266861	<i>alr</i>	alanine racemase, biosynthetic, PLP-binding	1464	329
b4054	4267114	4268307	<i>tyrB</i>	tyrosine aminotransferase, tyrosine-repressible, PLP-dependent	1881	697
b4055	4269414	4270127	<i>aphA</i>	acid phosphatase/phosphotransferase, class B, non-specific	5819	839
b4056	4270238	4270654	<i>yjbQ</i>	thiamine phosphate synthase	1910	2551
b4057	4270658	4271014	<i>yjbR</i>	DUF419 family protein	695	599
b4058	4273871	4271049	<i>uvrA</i>	ATPase and DNA damage recognition protein of nucleotide excision repair excinuclease UvrABC	5618	1630

b4059	4274125	4274661	<i>ssb</i>	single-stranded DNA-binding protein	5442	1228
b4060	4275041	4274760	<i>yjcB</i>	putative inner membrane protein	79	224
b4061	4275471	4277057	<i>yjcC</i>	putative membrane-anchored cyclic-di-GMP phosphodiesterase	510	1021
b4062	4277383	4277060	<i>soxS</i>	superoxide response regulon transcriptional activator; autoregulator	1673	1996
b4063	4277469	4277933	<i>soxR</i>	redox-sensitive transcriptional activator of <i>soxS</i> ; autorepressor	301	157
b4064	4278479	4279828	<i>ghxP</i>	guanine/hypoxanthine permease, high affinity; guanine/hypoxanthine:H ⁺ symporter	184	191
b4065	4279980	4281629	<i>yjcE</i>	putative cation/proton antiporter	836	343
b4066	4283075	4281783	<i>yjcF</i>	pentapeptide repeats protein	65	2913
b4067	4284902	4283253	<i>actP</i>	acetate transporter	2556	1050
b4068	4285213	4284899	<i>yjcH</i>	DUF485 family inner membrane protein	620	201
b4069	4287371	4285413	<i>acs</i>	acetyl-CoA synthetase	16377	4013
b4070	4287764	4289200	<i>nrfA</i>	nitrite reductase, formate-dependent, cytochrome	880	383
b4071	4289245	4289811	<i>nrfB</i>	nitrite reductase, formate-dependent, penta-heme cytochrome c	152	71
b4072	4289808	4290479	<i>nrfC</i>	formate-dependent nitrite reductase, 4Fe4S subunit	82	28
b4073	4290476	4291432	<i>nrfD</i>	formate-dependent nitrite reductase, membrane subunit	76	67
b4074	4291512	4293170	<i>nrfE</i>	heme lyase (NrfEFG) for insertion of heme into c552, subunit NrfE	41	211
b4075	4293163	4293546	<i>nrfF</i>	heme lyase (NrfEFG) for insertion of heme into c552, subunit NrfF	10	72
b4076	4293543	4294139	<i>nrfG</i>	heme lyase (NrfEFG) for insertion of heme into c552, subunit NrfG	27	53
b4077	4294481	4295794	<i>gltP</i>	glutamate/aspartate:proton symporter	920	572
b4078	4297125	4296436	<i>yjcO</i>	Sell family TPR-like repeat protein	1007	1003
b4079	4299366	4297219	<i>fdhF</i>	formate dehydrogenase-H, selenopolypeptide subunit	1496	1152
b4080	4301030	4299564	<i>mdtP</i>	outer membrane factor of efflux pump	21	122
b4081	4303078	4301027	<i>mdtO</i>	membrane translocase (MDR) of MdtNOP efflux pump, PET family	64	168
b4082	4304109	4303078	<i>mdtN</i>	membrane fusion protein of efflux pump	89	100
b4083	4306597	4304612	<i>yjcS</i>	metallo-beta-lactamase superfamily protein	15	91
b4084	4307799	4306870	<i>alsK</i>	D-allose kinase	177	180
b4085	4308478	4307783	<i>alsE</i>	allulose-6-phosphate 3-epimerase	142	142
b4086	4309469	4308489	<i>alsC</i>	D-allose ABC transporter permease	182	165
b4087	4310980	4309448	<i>alsA</i>	D-allose ABC transporter ATPase	199	351
b4088	4312042	4311107	<i>alsB</i>	D-allose ABC transporter periplasmic binding protein	440	160
b4089	4312991	4312101	<i>alsR</i>	d-allose-inducible als operon transcriptional repressor; autorepressor; repressor of <i>rpiR</i>	2115	919
b4090	4313350	4313799	<i>rpiB</i>	ribose 5-phosphate isomerase B/allose 6-phosphate isomerase	94	138
b4092	4315102	4314344	<i>phnP</i>	5-phospho-alpha-D-ribosyl 1,2-cyclic phosphate phosphodiesterase	110	85
b4093	4315538	4315104	<i>phnO</i>	aminoalkylphosphonate N-acetyltransferase	68	30
b4094	4316082	4315525	<i>phnN</i>	ribose 1,5-bisphosphokinase	69	18
b4095	4317218	4316082	<i>phnM</i>	ribophosphonate triphosphate hydrolase	147	36
b4096	4317895	4317215	<i>phnL</i>	ribophosphonate triphosphate synthase subunit; putative ABC transporter-related ATPase	116	31
b4097	4318764	4318006	<i>phnK</i>	carbon-phosphorus lyase complex subunit, putative ATP transporter ATP-binding protein	126	29
b4098	4319606	4318761	<i>phnJ</i>	carbon-phosphorus lyase, SAM-dependent	169	37
b4099	4320663	4319599	<i>phnI</i>	ribophosphonate triphosphate synthase complex putative catalytic subunit	246	89
b4100	4321247	4320663	<i>phnH</i>	ribophosphonate triphosphate synthase subunit	96	20
b4101	4321696	4321244	<i>phnG</i>	ribophosphonate triphosphate synthase subunit	65	12
b4102	4322422	4321697	<i>phnF</i>	putative DNA-binding transcriptional regulator of phosphonate uptake and biodegradation	213	29
b4105	4324352	4323336	<i>phnD</i>	phosphonate ABC transporter periplasmic binding protein	3018	327

b4106	4325165	4324377	<i>phnC</i>	phosphonate ABC transporter ATPase	749	92
b4107	4325741	4325298	<i>yjdN</i>	metalloprotein superfamily protein	350	1425
b4108	4326734	4326399	<i>yjdM</i>	zinc-ribbon family protein	177	169
b4109	4327135	4329363	<i>crfC</i>	clamp-binding sister replication fork colocalization protein, dynamin-related	1078	4679
b4110	4329360	4330238	<i>yjcZ</i>	YjcZ family protein; yjhH motility defect suppressor	478	446
b4111	4330502	4332004	<i>proP</i>	proline/glycine betaine transporter	5506	3458
b4112	4333272	4332181	<i>basS</i>	sensory histidine kinase in two-component regulatory system with BasR	4216	7064
b4113	4333950	4333282	<i>basR</i>	response regulator in two-component regulatory system with BasS	5210	2174
b4114	4335590	4333947	<i>eptA</i>	lipid A phosphoethanolamine transferase	5131	3092
b4115	4337031	4335694	<i>adiC</i>	arginine:agmatine antiporter	177	115
b4116	4337929	4337168	<i>adiY</i>	adi system transcriptional activator	1460	465
b4117	4340521	4338254	<i>adiA</i>	arginine decarboxylase	798	513
b4118	4341628	4340720	<i>melR</i>	melibiose operon transcriptional regulator; autoregulator	7697	2440
b4119	4341911	4343266	<i>mela</i>	alpha-galactosidase, NAD(P)-binding	296	179
b4120	4343369	4344790	<i>melB</i>	melibiose:sodium symporter	360	2652
b4121	4345558	4344929	<i>yjdF</i>	DUF2238 family inner membrane protein	75	159
b4122	4347326	4345680	<i>fumB</i>	anaerobic class I fumarate hydratase (fumarase B)	1520	210
b4123	4348744	4347404	<i>dcuB</i>	C4-dicarboxylate transporter, anaerobic; DcuS co-sensor	1581	415
b4124	4350034	4349315	<i>dcuR</i>	response regulator in two-component regulatory system with DcuS	1485	1090
b4125	4351662	4350031	<i>dcuS</i>	sensory histidine kinase in two-component regulatory system with DcuR, regulator of anaerobic fumarate respiration	1181	1872
b4126	4351843	4352073	<i>yjdI</i>	putative 4Fe-4S mono-cluster protein	193	77
b4127	4352085	4352357	<i>yjdJ</i>	GNAT family putative N-acetyltransferase	962	1198
b4128	4352584	4352880	<i>ghoS</i>	antitoxin of GhoTS toxin-antitoxin pair; endonuclease for ghoT mRNA	163	186
b4129	4354717	4353200	<i>lysU</i>	lysine tRNA synthetase, inducible	2277	876
b4130	4356411	4354954	<i>dtpC</i>	dipeptide and tripeptide permease	113	347
b4131	4358617	4356470	<i>cadA</i>	lysine decarboxylase, acid-inducible	66	307
b4132	4360031	4358697	<i>cadB</i>	putative lysine/cadaverine transporter	37	250
b4133	4361934	4360396	<i>cadC</i>	cadBA operon transcriptional activator	512	1251
b4135	4363308	4362733	<i>yjdC</i>	putative transcriptional regulator	1466	1548
b4136	4365042	4363345	<i>dsbD</i>	thiol:disulfide interchange protein and activator of DsbC	563	788
b4137	4365356	4365018	<i>cutA</i>	divalent-cation tolerance protein, copper sensitivity	441	777
b4138	4366773	4365472	<i>dcuA</i>	C4-dicarboxylate antiporter	12209	4667
b4139	4368327	4366891	<i>aspA</i>	aspartate ammonia-lyase	225094	62839
b4140	4368664	4369140	<i>fxsA</i>	suppressor of F exclusion of phage T7	1671	1898
b4141	4370412	4369156	<i>yjeH</i>	putative transporter	180	700
b4142	4370688	4370981	<i>groS</i>	Cpn10 chaperonin GroES, small subunit of GroESL	11243	2062
b4143	4371025	4372671	<i>groL</i>	Cpn60 chaperonin GroEL, large subunit of GroESL	90649	21897
b4144	4372809	4373162	<i>yjeI</i>	DUF4156 family lipoprotein	1692	694
b4145	4374234	4373365	<i>yjeJ</i>	uncharacterized protein	171	261
b4146	4375657	4374629	<i>epmB</i>	EF-P-Lys34 lysylation protein; weak lysine 2,3-aminomutase	501	754
b4147	4375699	4376265	<i>efp</i>	polyproline-specific translation elongation factor EF-P	7458	1866
b4148	4376875	4377192	<i>sugE</i>	multidrug efflux system protein	236	507
b4149	4377722	4377189	<i>blc</i>	outer membrane lipoprotein cell division and growth lipocalin	1485	1533
b4150	4378944	4377811	<i>ampC</i>	penicillin-binding protein; beta-lactamase, intrinsically weak	593	492
b4151	4379366	4379007	<i>frdD</i>	fumarate reductase (anaerobic), membrane anchor subunit	4106	565
b4152	4379772	4379377	<i>frdC</i>	fumarate reductase (anaerobic), membrane anchor subunit	6979	798

b4153	4380517	4379783	<i>frdB</i>	fumarate reductase (anaerobic), Fe-S subunit	13519	1130
b4154	4382318	4380510	<i>frdA</i>	anaerobic fumarate reductase catalytic and NAD/flavoprotein subunit	48414	3649
b4155	4382643	4383620	<i>epmA</i>	Elongation Factor P Lys34 lysyltransferase	297	410
b4156	4383839	4385341	<i>yjeM</i>	putative transporter	418	338
b4157	4385393	4385707	<i>yjeN</i>	uncharacterized protein	24	38
b4158	4385704	4386018	<i>yjeO</i>	inner membrane protein	53	244
b4159	4389370	4386047	<i>mscM</i>	mechanosensitive channel protein, miniconductance	812	822
b4160	4390360	4389392	<i>psd</i>	phosphatidylserine decarboxylase	2288	1687
b4161	4391509	4390457	<i>rsgA</i>	ribosome small subunit-dependent GTPase A	2143	1520
b4162	4391604	4392149	<i>orn</i>	oligoribonuclease	1853	622
b4166	4394067	4392928	<i>queG</i>	epoxyqueuosine reductase, cobalamine-stimulated; queosine biosynthesis	691	1467
b4167	4394066	4395613	<i>nnr</i>	bifunctional NAD(P)H-hydrate repair enzyme; C-terminal domain ADP-dependent (S)-NAD(P)H-hydrate dehydratase and N-terminal domain NAD(P)H-hydrate epimerase	862	551
b4168	4395585	4396046	<i>tsaE</i>	tRNA(ANN) t(6)A37 threonylcarbamoyladenine modification protein; ADP binding protein	272	190
b4169	4396065	4397402	<i>amiB</i>	N-acetylmuramoyl-L-alanine amidase II	942	1028
b4170	4397412	4399259	<i>mutL</i>	methyl-directed mismatch repair protein	1053	1605
b4171	4399252	4400202	<i>miaA</i>	delta(2)-isopentenylpyrophosphate tRNA-adenosine transferase	9404	5774
b4172	4400288	4400596	<i>hfq</i>	global sRNA chaperone; HF-I, host factor for RNA phage Q beta replication	14034	7679
b4173	4400672	4401952	<i>hflX</i>	GTPase, stimulated by 50S subunit binding; Mn(2+) homeostasis regulator	4344	3823
b4174	4402038	4403297	<i>hflK</i>	modulator for HflB protease specific for phage lambda cII repressor	7617	3525
b4175	4403300	4404304	<i>hflC</i>	HflB protease modulator specific for phage lambda cII repressor	7791	2896
b4176	4404386	4404583	<i>yjeT</i>	DUF2065 family protein	23	55
b4177	4404687	4405985	<i>purA</i>	adenylosuccinate synthetase	22486	13446
b4178	4406190	4406615	<i>nsrR</i>	nitric oxide-sensitive repressor for NO regulon	527	869
b4179	4406654	4409095	<i>rnr</i>	exoribonuclease R, RNase R	6602	4538
b4180	4409275	4410006	<i>rlmB</i>	23S rRNA mG2251 2'-O-ribose methyltransferase, SAM-dependent	824	376
b4181	4410133	4410534	<i>yjfI</i>	DUF2170 family protein	31	86
b4182	4410553	4411251	<i>yjfJ</i>	PspA/IM30 family protein	56	66
b4183	4411302	4411961	<i>yjfK</i>	DUF2491 family protein	20	73
b4184	4411979	4412377	<i>yjfL</i>	UPF0719 family inner membrane protein	5	36
b4185	4412387	4413025	<i>yjfM</i>	DUF1190 family protein	13	33
b4186	4413028	4414191	<i>yjfC</i>	ATP-Grasp family ATPase	19	85
b4187	4414275	4415900	<i>aidB</i>	DNA alkylation damage repair protein; flavin-containing DNA binding protein, weak isovaleryl CoA dehydrogenase	376	579
b4188	4416292	4416017	<i>yjfN</i>	DUF1471 family periplasmic protein	6876	696
b4189	4416770	4416441	<i>bsmA</i>	biofilm peroxide resistance protein	16084	1811
b4190	4416952	4417701	<i>yjfP</i>	acyl CoA esterase	161	254
b4191	4418453	4417698	<i>ulaR</i>	transcriptional repressor for the L-ascorbate utilization divergent operon	375	497
b4192	4419625	4418561	<i>ulaG</i>	L-ascorbate 6-phosphate lactonase	199	206
b4193	4419980	4421377	<i>ulaA</i>	L-ascorbate-specific enzyme IIC permease component of PTS	179	124
b4194	4421393	4421698	<i>ulaB</i>	L-ascorbate-specific enzyme IIB component of PTS	81	23
b4195	4421708	4422172	<i>ulaC</i>	L-ascorbate-specific enzyme IIA component of PTS	64	21
b4196	4422186	4422836	<i>ulaD</i>	3-keto-L-gulonate 6-phosphate decarboxylase	89	33
b4197	4422846	4423700	<i>ulaE</i>	L-xylulose 5-phosphate 3-epimerase	86	92
b4198	4423700	4424386	<i>ulaF</i>	L-ribulose 5-phosphate 4-epimerase	114	94

b4199	4424791	4424516	<i>yjfY</i>	YhcN family protein, periplasmic	49	606
b4200	4425118	4425513	<i>rpsF</i>	30S ribosomal subunit protein S6	22746	5275
b4201	4425520	4425834	<i>priB</i>	primosomal protein N	29013	7273
b4202	4425839	4426066	<i>rpsR</i>	30S ribosomal subunit protein S18	16238	4244
b4203	4426108	4426557	<i>rplI</i>	50S ribosomal subunit protein L9	20336	3521
b4204	4427422	4426628	<i>yjfZ</i>	uncharacterized protein	136	447
b4206	4428717	4428079	<i>ytfB</i>	OapA family protein	4220	4107
b4207	4428935	4429555	<i>fkfB</i>	FKBP-type peptidyl-prolyl cis-trans isomerase (rotamase)	4480	995
b4208	4429864	4431276	<i>cycA</i>	D-alanine/D-serine/glycine transporter	7497	1941
b4209	4431983	4431321	<i>ytfE</i>	iron-sulfur cluster repair protein RIC	291	159
b4210	4433056	4432091	<i>ytfF</i>	DMT transporter family inner membrane protein	182	157
b4211	4434024	4433164	<i>qorB</i>	NAD(P)H:quinone oxidoreductase	121	92
b4212	4434113	4434493	<i>ytfH</i>	DUF24 family HxlR-type putative transcriptional regulator	103	365
b4213	4436565	4434622	<i>cpdB</i>	2':3'-cyclic-nucleotide 2'-phosphodiesterase	4248	2341
b4214	4436755	4437495	<i>cysQ</i>	3'(2'),5'-bisphosphate nucleotidase	7009	6116
b4215	4437707	4438645	<i>ytfI</i>	uncharacterized protein	445	2657
b4216	4439262	4438708	<i>ytfJ</i>	putative transcriptional regulator	2680	2606
b4217	4439587	4439793	<i>ytfK</i>	DUF1107 family protein	4499	4876
b4218	4441215	4439872	<i>ytfL</i>	UPF0053 family inner membrane protein	673	1139
b4219	4442176	4441538	<i>msrA</i>	methionine sulfoxide reductase A	1509	1321
b4220	4442382	4444115	<i>tamA</i>	translocation and assembly module for autotransporter export, outer membrane subunit	993	957
b4221	4444112	4447891	<i>tamB</i>	translocation and assembly module for autotransporter export, inner membrane subunit	1519	1866
b4222	4447894	4448235	<i>ytfP</i>	GGCT-like protein	487	1115
b4224	4448447	4448698	<i>chpS</i>	antitoxin of the ChpBS toxin-antitoxin system	346	614
b4225	4448692	4449042	<i>chpB</i>	toxin of the ChpB-ChpS toxin-antitoxin system	295	191
b4226	4449652	4449122	<i>ppa</i>	inorganic pyrophosphatase	34513	6001
b4227	4449962	4450918	<i>ytfQ</i>	galactofuranose ABC transporter periplasmic binding protein	8574	1052
b4230	4452571	4453596	<i>ytfT</i>	putative sugar ABC transporter permease	393	57
b4231	4453583	4454578	<i>yjfF</i>	putative sugar ABC transporter permease	446	296
b4232	4455609	4454611	<i>fbp</i>	fructose-1,6-bisphosphatase I	20604	4309
b4233	4455785	4457158	<i>mpl</i>	UDP-N-acetylmuramate:L-alanyl-gamma-D-glutamyl-meso-diaminopimelate ligase	3459	1166
b4234	4457865	4457314	<i>yjgA</i>	ribosome-associated UPF0307 family protein	3306	4114
b4235	4457959	4459311	<i>pmbA</i>	putative antibiotic peptide MccB17 maturation peptidase	2673	1432
b4237	4460364	4459900	<i>nrdG</i>	anaerobic ribonucleotide reductase activating protein	166	139
b4238	4462660	4460522	<i>nrdD</i>	anaerobic ribonucleoside-triphosphate reductase	2757	1393
b4239	4464709	4463054	<i>treC</i>	trehalose-6-P hydrolase	25035	181
b4240	4466180	4464759	<i>treB</i>	trehalose-specific PTS enzyme: IIB and IIC component	106451	334
b4241	4467246	4466299	<i>treR</i>	trehalose 6-phosphate-inducible trehalose regulon transcriptional repressor	1432	478
b4242	4467625	4470321	<i>mgtA</i>	magnesium transporter	7090	3927
b4243	4470913	4470527	<i>ridA</i>	enamine/imine deaminase, reaction intermediate detoxification	12500	3927
b4244	4471447	4470986	<i>pyrI</i>	aspartate carbamoyltransferase, regulatory subunit	3259	503
b4245	4472395	4471460	<i>pyrB</i>	aspartate carbamoyltransferase, catalytic subunit	6333	814
b4246	4472533	4472399	<i>pyrL</i>	pyrBI operon leader peptide	6	42
b4248	4473209	4472814	<i>yjgH</i>	UPF0131 family protein	93	255
b4249	4474053	4473340	<i>bdcA</i>	c-di-GMP-binding biofilm dispersal mediator protein	155	158
b4251	4474124	4474717	<i>bdcR</i>	transcriptional repressor for divergent bdcA	310	407
b4252	4474862	4475314	<i>tabA</i>	biofilm modulator regulated by toxins; DUF386 family protein, cupin superfamily protein	716	291
b4253	4475437	4477251	<i>yjgL</i>	SopA-central-domain-like hexapeptide repeat protein	338	2224

b4254	4478311	4477307	<i>argI</i>	ornithine carbamoyltransferase 1	51	4912
b4255	4478473	4478889	<i>rraB</i>	protein inhibitor of RNase E	13288	13816
b4256	4479537	4479034	<i>yjgM</i>	GNAT family putative N-acetyltransferase	421	370
b4257	4479730	4480926	<i>yjgN</i>	DUF898 family inner membrane protein	23	492
b4258	4483837	4480982	<i>valS</i>	valyl-tRNA synthetase	7677	3086
b4259	4484280	4483837	<i>holC</i>	DNA polymerase III, chi subunit	226	296
b4260	4485951	4484440	<i>pepA</i>	multifunctional aminopeptidase A: a cyteinyglycinase, transcription regulator and site-specific recombination factor	3619	1750
b4261	4486218	4487318	<i>lptF</i>	lipopolysaccharide export ABC permease	1162	1095
b4262	4487318	4488400	<i>lptG</i>	lipopolysaccharide export ABC permease	1134	866
b4263	4490063	4488561	<i>yjgR</i>	DUF853 family protein with NTPase fold	1677	917
b4264	4491139	4490141	<i>idnR</i>	transcriptional repressor, 5-gluconate-binding	378	733
b4265	4492525	4491206	<i>idnT</i>	L-idonate and D-gluconate transporter	209	400
b4266	4493351	4492587	<i>idnO</i>	5-keto-D-gluconate-5-reductase	222	60
b4267	4494406	4493375	<i>idnD</i>	L-idonate 5-dehydrogenase, NAD-binding	572	331
b4268	4494623	4495186	<i>idnK</i>	D-gluconate kinase, thermosensitive	594	204
b4269	4496209	4495190	<i>ahr</i>	broad specificity NADPH-dependent aldehyde reductase, Zn-containing	787	276
b4272	4498272	4498637	<i>insC1</i>	IS2 repressor TnpA	403	429
b4273	4498595	4499500	<i>insD1</i>	IS2 transposase TnpB	652	819
b4277	4501260	4501589	<i>yjgZ</i>	uncharacterized protein	4	12
b4278	4503431	4502103	<i>insG</i>	IS4 transposase	572	2385
b4279	4504058	4505275	<i>yjhB</i>	putative MFS transporter, membrane protein	851	706
b4280	4505287	4506405	<i>yjhC</i>	GFO/IDH/MOCA family putative oxidoreductase. NAD(P)-dependent	2702	2691
b4284	4508617	4507466	<i>insI1</i>	IS30 transposase	629	1322
b4287	4511457	4510690	<i>fecE</i>	ferric citrate ABC transporter ATPase	2048	76
b4288	4512414	4511458	<i>fecD</i>	ferric citrate ABC transporter permease	522	50
b4289	4513409	4512411	<i>fecC</i>	ferric citrate ABC transporter permease	858	42
b4290	4514308	4513406	<i>fecB</i>	ferric citrate ABC transporter periplasmic binding protein	5697	184
b4291	4516677	4514353	<i>fecA</i>	TonB-dependent outer membrane ferric citrate transporter and signal transducer; ferric citrate extracellular receptor; FecR-interacting protein	25410	235
b4292	4517717	4516764	<i>fecR</i>	anti-sigma transmembrane signal transducer for ferric citrate transport; periplasmic FecA-bound ferric citrate sensor and cytoplasmic FecI ECF sigma factor activator	203	49
b4293	4518235	4517714	<i>fecI</i>	RNA polymerase sigma-19 factor, fec operon-specific; ECF sigma factor	385	449
b4294	4518527	4518802	<i>insA</i>	IS1 repressor TnpA	165	548
b4295	4520324	4519338	<i>yjhU</i>	putative DNA-binding transcriptional regulator; KpLE2 phage-like element	2281	1797
b4296	4522020	4520671	<i>yjhF</i>	putative transporter	102	590
b4297	4524094	4522127	<i>yjhG</i>	putative dehydratase	616	568
b4298	4525010	4524105	<i>yjhH</i>	putative lyase/synthase	396	230
b4299	4525803	4525015	<i>yjhI</i>	putative DNA-binding transcriptional regulator	464	336
b4300	4526888	4526106	<i>sgcR</i>	putative DNA-binding transcriptional regulator	230	454
b4301	4527537	4526905	<i>sgcE</i>	putative epimerase	117	100
b4302	4527980	4527549	<i>sgcA</i>	putative phosphotransferase enzyme IIA component	132	97
b4303	4528917	4528111	<i>sgcQ</i>	putative nucleoside triphosphatase	163	328
b4304	4530243	4528930	<i>sgcC</i>	putative PTS system EIIC permease component	202	349
b4305	4531651	4530530	<i>sgcX</i>	putative endoglucanase with Zn-dependent exopeptidase domain	847	670
b4306	4533183	4532437	<i>yjhP</i>	putative methyltransferase	255	139
b4307	4533784	4533239	<i>yjhQ</i>	GNAT family putative N-acetyltransferase	260	104
b4309	4537594	4536614	<i>nanS</i>	9-O-acetyl N-acetylneuraminic acid esterase	70	239
b4310	4538765	4537659	<i>nanM</i>	N-acetylneuraminic acid mutarotase	435	802

b4311	4539501	4538785	<i>nanC</i>	N-acetylnuraminic acid outer membrane channel protein	143	271
b4312	4540957	4541559	<i>fimB</i>	tyrosine recombinase/inversion of on/off regulator of fimA	217	722
b4313	4542037	4542633	<i>fimE</i>	tyrosine recombinase/inversion of on/off regulator of fimA	79	493
b4314	4543115	4543663	<i>fimA</i>	major type 1 subunit fimbriae (pilin)	73226	23499
b4315	4543728	4544267	<i>fimI</i>	fimbrial protein involved in type 1 pilus biosynthesis	925	1559
b4316	4544304	4545029	<i>fimC</i>	periplasmic chaperone	1078	1329
b4317	4545096	4547732	<i>fimD</i>	fimbrial usher outer membrane porin protein; FimCD chaperone-usher	2246	2496
b4318	4547742	4548272	<i>fimF</i>	minor component of type 1 fimbriae	477	258
b4319	4548285	4548788	<i>fimG</i>	minor component of type 1 fimbriae	477	325
b4320	4548808	4549710	<i>fimH</i>	minor component of type 1 fimbriae	954	736
b4321	4551296	4549953	<i>gntP</i>	fructuronate transporter	598	463
b4322	4551636	4552820	<i>uxuA</i>	mannonate hydrolase	2253	542
b4323	4552901	4554361	<i>uxuB</i>	D-mannonate oxidoreductase, NAD-dependent	635	167
b4324	4554576	4555349	<i>uxuR</i>	fructuronate-inducible hexuronate regulon transcriptional repressor; autorepressor	765	610
b4325	4556320	4555490	<i>yjiC</i>	uncharacterized protein	16	146
b4326	4556993	4557385	<i>iraD</i>	RpoS stabilizer after DNA damage, anti-RssB factor	587	248
b4327	4558289	4557378	<i>hypT</i>	hypochlorite-responsive transcription factor	360	539
b4328	4559526	4558354	<i>iadA</i>	isoaspartyl dipeptidase	1627	263
b4329	4560000	4559539	<i>yjiG</i>	SpmB family inner membrane protein	29	142
b4330	4560680	4559997	<i>yjiH</i>	nucleoside recognition pore and gate family putative inner membrane transporter	20	180
b4331	4560930	4561484	<i>kptA</i>	RNA 2'-phosphotransferase	532	803
b4332	4562675	4561497	<i>yjiJ</i>	DUF1228 family putative inner membrane MFS superfamily transporter	285	462
b4333	4563603	4562743	<i>yjiK</i>	SdiA-regulated family putative membrane-anchored protein; putative phytase-like esterase	176	551
b4334	4564689	4563922	<i>yjiL</i>	putative ATPase, activator of (R)-hydroxyglutaryl-CoA dehydratase	170	41
b4335	4565850	4564699	<i>yjiM</i>	putative 2-hydroxyglutaryl-CoA dehydratase	1523	220
b4336	4567246	4565966	<i>yjiN</i>	zinc-type alcohol dehydrogenase-like protein	226	545
b4337	4568519	4567287	<i>mdtM</i>	multidrug efflux system protein	259	284
b4340	4571574	4570162	<i>yjiR</i>	putative DNA-binding transcriptional regulator/putative aminotransferase	384	319
b4341	4571751	4571915	<i>yjiS</i>	DUF1127 family protein	1	13
b4345	4577958	4576912	<i>mcrC</i>	5-methylcytosine-specific restriction enzyme McrBC, subunit McrC	288	879
b4346	4579337	4577958	<i>mcrB</i>	5-methylcytosine-specific restriction enzyme McrBC, subunit McrB	1836	1892
b4347	4579840	4579499	<i>symE</i>	toxic peptide regulated by antisense sRNA symR	17	47
b4348	4581462	4580068	<i>hsdS</i>	specificity determinant for hsdM and hsdR	1130	897
b4349	4583048	4581459	<i>hsdM</i>	DNA methyltransferase M	1121	679
b4350	4586761	4583249	<i>hsdR</i>	endonuclease R Type I restriction enzyme	9908	3082
b4351	4586949	4587863	<i>mrr</i>	methylated adenine and cytosine restriction protein	1962	990
b4352	4588865	4587909	<i>yjiA</i>	metal-binding GTPase	1536	500
b4353	4589079	4588876	<i>yjiX</i>	DUF466 family protein	106	113
b4354	4591279	4589129	<i>yjiY</i>	putative transporter	7502	136
b4355	4591657	4593312	<i>tsr</i>	methyl-accepting chemotaxis protein I, serine sensor receptor	6563	1868
b4356	4594722	4593361	<i>lgoT</i>	putative L-galactonate:H ⁺ symporter	1327	896
b4357	4595851	4594937	<i>lgoR</i>	putative transcriptional activator for L-galactonate catabolism	6292	754
b4358	4595990	4597012	<i>lgoD</i>	L-galactonate oxidoreductase; L-gulonate oxidoreductase	23	206
b4359	4599441	4597150	<i>opgB</i>	OPG periplasmic biosynthetic phosphoglycerol transferases I (membrane-bound) and II (soluble)	2812	2719
b4360	4600189	4599695	<i>yjiA</i>	putative DUF2501 family periplasmic protein	807	776

b4361	4600975	4600238	<i>dnaC</i>	DNA biosynthesis protein	489	331
b4362	4601517	4600978	<i>dnaT</i>	DNA biosynthesis protein (primosomal protein I)	221	311
b4363	4602097	4601624	<i>yjjB</i>	DUF3815 family inner membrane protein	52	57
b4364	4602858	4602088	<i>yjjP</i>	DUF1212 family inner membrane protein	573	620
b4365	4603477	4604202	<i>yjjQ</i>	putative transcriptional regulator	5	70
b4366	4604160	4604837	<i>bglJ</i>	bgl operon transcriptional activator	58	410
b4367	4605663	4604875	<i>fhuF</i>	ferric iron reductase involved in ferric hydroximate transport	2117	1761
b4371	4607700	4606669	<i>rsmC</i>	16S rRNA m(2)G1207 methyltransferase, SAM-dependent	691	486
b4372	4607803	4608216	<i>holD</i>	DNA polymerase III, psi subunit	149	205
b4373	4608185	4608631	<i>rimI</i>	ribosomal-protein-S18-alanine N-acetyltransferase	212	268
b4374	4608646	4609323	<i>yjjG</i>	dUMP phosphatase	517	343
b4375	4609414	4611003	<i>prfC</i>	peptide chain release factor RF-3	4459	1759
b4376	4611396	4612001	<i>osmY</i>	salt-inducible putative ABC transporter periplasmic binding protein	8865	6948
b4377	4612411	4613484	<i>yjjU</i>	putative patatin-like family phospholipase	239	242
b4378	4613481	4614260	<i>yjjV</i>	putative DNase	108	67
b4379	4615543	4614680	<i>yjjW</i>	putative pyruvate formate lyase activating enzyme	1054	71
b4380	4617065	4615515	<i>yjiI</i>	DUF3029 family protein, putative glycine radical enzyme	16206	4982
b4381	4617323	4618102	<i>deoC</i>	2-deoxyribose-5-phosphate aldolase, NAD(P)-linked	57338	11249
b4382	4618229	4619551	<i>deoA</i>	thymidine phosphorylase	67320	11649
b4383	4619603	4620826	<i>deoB</i>	phosphopentomutase	55327	9565
b4384	4620883	4621602	<i>deoD</i>	purine nucleoside phosphorylase I; nicotinamide 1-beta-D-ribose phosphorylase	52017	9544
b4385	4621769	4623100	<i>yjiJ</i>	putative protein kinase	550	661
b4386	4624117	4623101	<i>lplA</i>	lipoate-protein ligase A	498	147
b4387	4624789	4624145	<i>ytjB</i>	SMP_2 family putative membrane-anchored periplasmic protein	169	198
b4388	4624895	4625863	<i>serB</i>	3-phosphoserine phosphatase	344	239
b4389	4625912	4627294	<i>radA</i>	DNA repair protein	671	310
b4390	4627315	4628547	<i>nadR</i>	trifunctional protein: nicotinamide mononucleotide adenyltransferase, ribosylnicotinamide kinase, transcriptional repressor	1527	1661
b4391	4630522	4628855	<i>ettA</i>	energy-dependent translational throttle A	12016	2543
b4392	4630733	4632670	<i>slt</i>	lytic murein transglycosylase, soluble	2178	1764
b4393	4632760	4633086	<i>trpR</i>	transcriptional repressor, tryptophan-binding	183	338
b4394	4633745	4633233	<i>yjiX</i>	non-canonical purine NTP phosphatase, ITPase/XTPase	208	219
b4395	4633797	4634444	<i>ytjC</i>	phosphatase	740	462
b4396	4635310	4634441	<i>rob</i>	right oriC-binding transcriptional activator, AraC family	8326	3784
b4397	4635521	4635994	<i>creA</i>	putative periplasmic protein	549	537
b4398	4636007	4636696	<i>creB</i>	response regulator in two-component regulatory system with CreC	163	188
b4399	4636696	4638120	<i>creC</i>	sensory histidine kinase in two-component regulatory system with CreB or PhoB	191	383
b4400	4638178	4639530	<i>creD</i>	inner membrane protein	193	774
b4401	4640306	4639590	<i>arcA</i>	response regulator in two-component regulatory system with ArcB or CpxA	23912	6779
b4402	4640402	4640542	<i>yjiY</i>	uncharacterized protein	392	793
b4403	4640942	4641628	<i>yjtD</i>	putative methyltransferase	425	428
b4406	214125	213925	<i>yaeP</i>	UPF0253 family protein	1850	974
b4407	4192837	4192637	<i>thiS</i>	immediate sulfur donor in thiazole formation	8	34
b4409	1704551	1704676	<i>blr</i>	beta-lactam resistance membrane protein; divisome-associated protein	82	71
b4410	4376317	4376442	<i>ecnA</i>	entericidin A membrane lipoprotein, antidote entericidin B	31	21
b4411	4376553	4376699	<i>ecnB</i>	entericidin B membrane lipoprotein	1383	1757
b4412	16903	16751	<i>hokC</i>	toxic membrane protein, small	142	21

b4415	607836	607988	<i>hokE</i>	toxic polypeptide, small	1	17
b4419	1269275	1269168	<i>ldrA</i>	toxic polypeptide, small	27	12
b4421	1269810	1269703	<i>ldrB</i>	toxic polypeptide, small	1	5
b4423	1270345	1270238	<i>ldrC</i>	toxic polypeptide, small	27	12
b4428	1492071	1491922	<i>hokB</i>	toxic polypeptide, small	176	171
b4453	3700087	3699980	<i>ldrD</i>	toxic polypeptide, small	11	28
b4455	3720600	3720448	<i>hokA</i>	toxic polypeptide, small	5	19
b4460	1983540	1982554	<i>araH</i>	L-arabinose ABC transporter permease	377	811
b4461	2748774	2750060	<i>yfiD</i>	UPF0053 family inner membrane protein	805	695
b4463	2899418	2897964	<i>ygcU</i>	putative FAD-linked oxidoreductase	89	150
b4464	3027121	3028488	<i>ghxQ</i>	guanine/hypoxanthine permease, high affinity; guanine/hypoxanthine:H ⁺ symporter	119	360
b4465	3077456	3076179	<i>yggP</i>	putative Zn-binding dehydrogenase	19	136
b4466	3119112	3114550	<i>sslE</i>	putative secreted and surface-associated lipoprotein mucinase	251	664
b4467	3125459	3124236	<i>glcF</i>	glycolate oxidase 4Fe-4S iron-sulfur cluster subunit	716	2495
b4468	3126522	3125470	<i>glcE</i>	glycolate oxidase FAD binding subunit	337	1476
b4469	3161146	3158927	<i>ygiQ</i>	Radical SAM superfamily protein	2038	1106
b4470	3256651	3255341	<i>yhaM</i>	putative L-serine dehydratase alpha chain	4343	378
b4471	3259649	3258285	<i>tdcG</i>	L-serine dehydratase 3, anaerobic	3100	410
b4472	3396258	3392458	<i>yhdP</i>	DUF3971-AsmA2 domains protein	1968	1753
b4473	3433560	3432436	<i>smf</i>	DNA recombination-mediator A family protein	984	2977
b4474	3502340	3503170	<i>frlC</i>	fructoselysine 3-epimerase	68	99
b4475	3556849	3555833	<i>rtcA</i>	RNA 3'-terminal phosphate cyclase	104	125
b4476	3577061	3575721	<i>gntU</i>	gluconate transporter, low affinity GNT 1 system	303	185
b4477	3873612	3872995	<i>dgoA</i>	2-oxo-3-deoxygalactonate 6-phosphate aldolase	50	18
b4478	3872998	3871850	<i>dgoD</i>	D-galactonate dehydratase	109	77
b4479	3875160	3874471	<i>dgoR</i>	D-galactonate catabolism operon transcriptional repressor	619	156
b4480	3947967	3947128	<i>hdfR</i>	flhDC operon transcriptional repressor	605	847
b4481	3977525	3978604	<i>wecF</i>	TDP-Fuc4NAc:lipidII Fuc4NAc transferase	723	553
b4482	4001056	4000292	<i>yigE</i>	DUF2233 family protein	58	204
b4483	4023554	4024336	<i>tatD</i>	quality control of Tat-exported FeS proteins; Mg- dependent cytoplasmic DNase	453	541
b4484	4105820	4106320	<i>cpxP</i>	inhibitor of the cpx response; periplasmic adaptor protein	295	53403
b4485	4451058	4452560	<i>ytfR</i>	putative sugar ABC transporter ATPase	1415	202
b4487	4313868	4314197	<i>yjdP</i>	putative periplasmic protein	454	257
b4501	2476310	2476510	<i>torI</i>	response regulator inhibitor for tor operon	51	574
b4502	2265295	2265041	<i>yeiW</i>	UPF0153 cysteine cluster protein	69	40
b4504	264247	264026	<i>ykhH</i>	uncharacterized protein	10	18
b4506	312514	312374	<i>ykgO</i>	RpmJ-like protein	4	3
b4509	573730	573870	<i>ylcG</i>	uncharacterized protein, DLP12 prophage	1	5
b4510	578327	578509	<i>rzoD</i>	DLP12 prophage; putative lipoprotein	22	31
b4511	613942	614160	<i>ybdZ</i>	stimulator of EntF adenylation activity, MbtH-like	73	15
b4512	632182	632379	<i>ybdD</i>	DUF466 family protein	131	213
b4513	728821	728732	<i>kdpF</i>	potassium ion accessory transporter subunit	0	21
b4515	774196	774309	<i>cydX</i>	cytochrome d (bd-I) ubiquinol oxidase subunit X	1195	987
b4516	1049833	1050108	<i>insA</i>	IS1 repressor TnpA	27	60
b4517	1052067	1052240	<i>gnsA</i>	putative phosphatidylethanolamine synthesis regulator	203	251
b4518	1068081	1068254	<i>ymdF</i>	KGG family protein	238	1751
b4520	1218983	1219201	<i>ymgF</i>	inner membrane division septum protein	18	50
b4522	1335124	1335288	<i>ymiA</i>	uncharacterized protein	31	90
b4523	1335291	1335458	<i>yciX</i>	uncharacterized protein	149	867
b4526	1418008	1417838	<i>ydaE</i>	conserved protein, Rac prophage	1	36
b4527	1419311	1419156	<i>ydaF</i>	uncharacterized protein, Rac prophage	5	24

b4528	1423400	1423585	<i>rzoR</i>	Rac prophage; putative lipoprotein	16	18
b4529	1441058	1441324	<i>ydbJ</i>	DUF333 family putative lipoprotein	700	367
b4532	1509286	1509462	<i>hicA</i>	mRNA interferase toxin of the HicAB toxin-antitoxin system	22	17
b4533	1636756	1636989	<i>ynfO</i>	uncharacterized protein, Qin prophage	26	70
b4535	1805165	1805272	<i>yniD</i>	uncharacterized protein	9	27
b4536	1908925	1909164	<i>yobH</i>	uncharacterized protein	428	861
b4537	1987758	1987507	<i>yecJ</i>	DUF2766 family protein	637	860
b4539	2089465	2089211	<i>yoeB</i>	toxin of the YoeB-YefM toxin-antitoxin system	1679	2337
b4541	2203972	2204289	<i>yehK</i>	uncharacterized protein	3	81
b4542	2215657	2215764	<i>yohO</i>	putative membrane protein	3	5
b4544	2372557	2372892	<i>arnE</i>	undecaprenyl phosphate-alpha-L-ara4N exporter; flippase ArnEF subunit	314	320
b4546	2528159	2527941	<i>ypeB</i>	DUF3820 family protein	187	70
b4547	2592762	2592962	<i>ypfN</i>	putative membrane protein, UPF0370 family	352	375
b4548	2776877	2777077	<i>ypjJ</i>	uncharacterized protein	4	10
b4550	3438649	3438431	<i>arfA</i>	alternate ribosome-rescue factor A	582	10822
b4551	3478792	3478592	<i>yheV</i>	DUF2387 family putative metal-binding protein	566	182
b4553	3725712	3725413	<i>ysaB</i>	uncharacterized protein	175	450
b4554	3776380	3776171	<i>yibT</i>	uncharacterized protein	3611	6529
b4555	3840215	3840508	<i>yicS</i>	putative periplasmic protein	103	395
b4557	3884816	3885073	<i>yidD</i>	membrane protein insertion efficiency factor, UPF0161 family inner membrane protein	390	219
b4558	3994522	3994725	<i>yifL</i>	putative lipoprotein	1956	2344
b4559	4352908	4353081	<i>ghoT</i>	toxin of GhoTS toxin-antitoxin pair; membrane-lytic protein; stimulator of persister cell formation	19	33
b4565	4530533	4530255	<i>sgcB</i>	putative enzyme IIB component of PTS	83	67
b4566	4534053	4533796	<i>yjhX</i>	UPF0386 family protein	140	556
b4567	4605804	4606040	<i>yjjZ</i>	uncharacterized protein	64	591
b4568	4612128	4612289	<i>ytjA</i>	uncharacterized protein	1304	1731
b4572	548357	549616	<i>ylbE</i>	NO-induced DUF1116 protein	21	61
b4586	238736	238257	<i>ykfM</i>	lethality reduction protein, putative inner membrane protein	25	629
b4588	572368	572469	<i>ylcH</i>	uncharacterized protein, DLP12 prophage	0	0
b4589	580445	580251	<i>ylcI</i>	DUF3950 family protein, DLP12 prophage	17	42
b4590	720583	720840	<i>ybfK</i>	uncharacterized protein	5	26
b4592	1040445	1040537	<i>cbdX</i>	putative cytochrome bd-II oxidase subunit	1	15
b4593	1223163	1222990	<i>ymgI</i>	uncharacterized protein	127	1093
b4594	1223264	1223449	<i>ymgJ</i>	uncharacterized protein	4	116
b4595	1308788	1308961	<i>yciY</i>	uncharacterized protein	1370	2486
b4596	1344609	1344436	<i>yciZ</i>	uncharacterized protein	91	309
b4598	1517194	1517099	<i>yncL</i>	stress-induced small inner membrane enterobacterial protein	29	198
b4599	1622646	1622741	<i>yneM</i>	inner membrane-associated protein	37	1875
b4601	1671777	1671860	<i>ydgU</i>	stationary phase-induced protein	2	51
b4602	1737545	1737456	<i>ynhF</i>	stress response membrane	41	238
b4606	2590866	2590807	<i>ypfM</i>	stress-induced small enterobacterial protein	0	0
b4613	3647788	3647705	<i>dinQ</i>	UV-inducible membrane toxin, DinQ-AgrB type I toxin-antitoxin system	0	1
b4618	3853553	3853642	<i>tisB</i>	toxic membrane persister formation peptide, LexA-regulated	1	10
b4620	4240055	4239777	<i>yjbT</i>	putative periplasmic protein	38	1077
b4621	4269012	4268809	<i>yjbS</i>	uncharacterized protein	1	17
b4622	4304403	4304128	<i>ytcA</i>	putative inner membrane efflux pump-associated DUF1656 family protein	3	8
b4637	710725	710639	<i>uof</i>	ryhB-regulated fur leader peptide	6	41
b4655	4506448	4506573	<i>ythA</i>	uncharacterized protein	0	30

b4662	77388	77519	<i>sgrT</i>	inhibitor of glucose uptake	6	23
b4663	1987959	1987873	<i>azuC</i>	acid-inducible small membrane-associated protein	2	48
b4664	3194766	3194825	<i>ibsD</i>	toxic membrane protein	0	2
b4666	3195141	3195200	<i>ibsE</i>	toxic membrane protein	0	3
b4667	2153408	2153349	<i>ibsA</i>	toxic membrane protein	0	1
b4668	2153737	2153681	<i>ibsB</i>	toxic membrane protein	0	1
b4671	313242	313141	<i>ykgR</i>	uncharacterized protein	1	1
b4675	1878874	1878948	<i>yoaJ</i>	inner membrane-associated protein	0	3
b4676	1878773	1878871	<i>yoaK</i>	inner membrane-associated protein	14	56
b4678	2087114	2087052	<i>yoeI</i>	uncharacterized protein	0	0
b4679	2228982	2229065	<i>yohP</i>	uncharacterized protein	1	4
b4680	2496921	2496992	<i>ypdK</i>	inner membrane protein	0	0
b4682	2905557	2905697	<i>yqcG</i>	membrane stress resistance protein	2	10
b4684	3032817	3032942	<i>yqfG</i>	uncharacterized protein	3	27
b4685	3307933	3307853	<i>yrbN</i>	uncharacterized protein	0	1
b4686	4053757	4053647	<i>yshB</i>	uncharacterized protein	19	30
b4687	2700197	2700117	<i>shoB</i>	toxic membrane protein	0	0
b4689	1639334	1639080	<i>rzoQ</i>	putative Rz1-like lipoprotein, Qin prophage	0	0
b4702	4467431	4467484	<i>mgtL</i>	regulatory leader peptide for mgtA	0	2
b4703	4332116	4332205	<i>pmrR</i>	putative membrane-bound BasS regulator	7	28
b4705	852997	852869	<i>mntS</i>	Mn(2)-response protein, MntR-repressed	234	1050